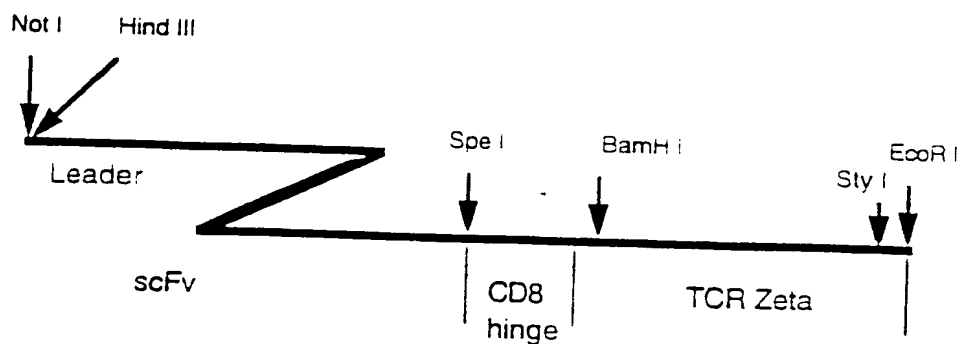
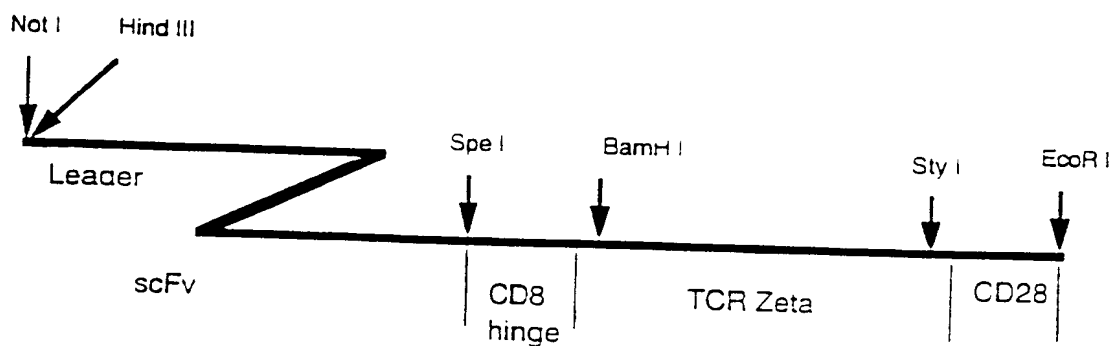
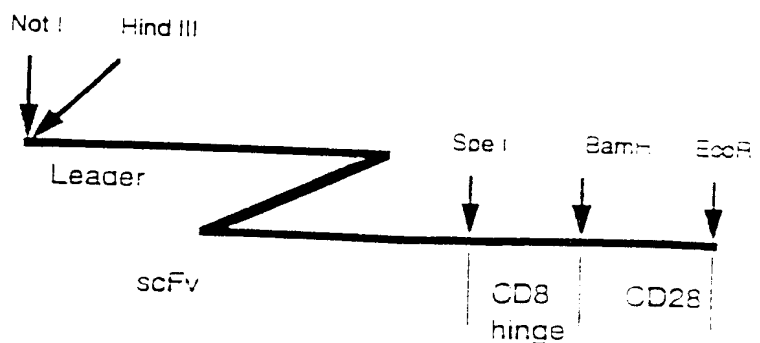


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FIG. 1

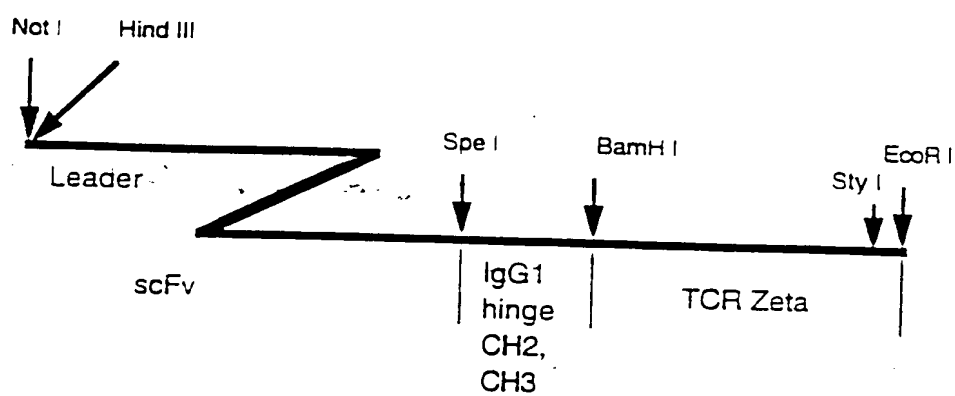
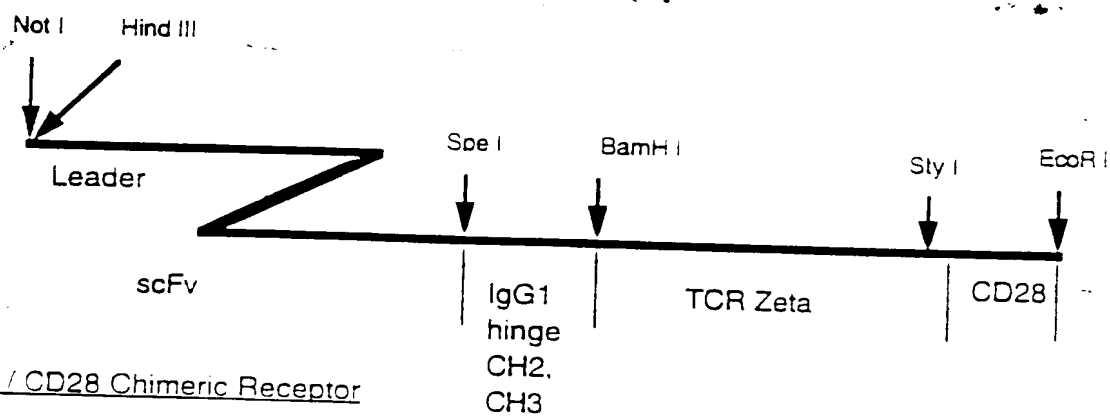
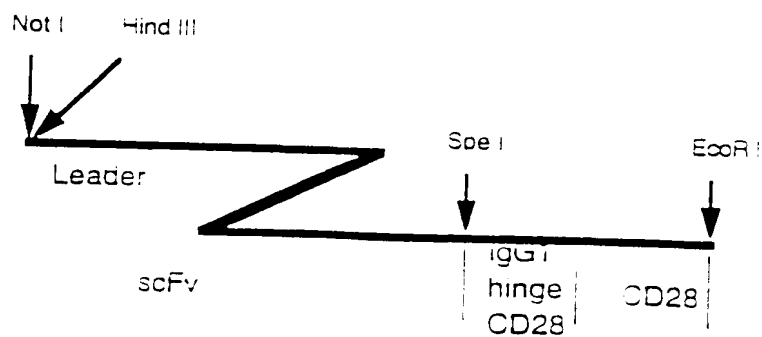
Construct cassettes cloned into pBluescript SK +

scFv / CD8 / Zeta Chimeric ReceptorscFv / CD8 / Zeta-CD28 fusion Chimeric ReceptorscFv / CD8 / CD28 Chimeric Receptor

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FIG. 2a

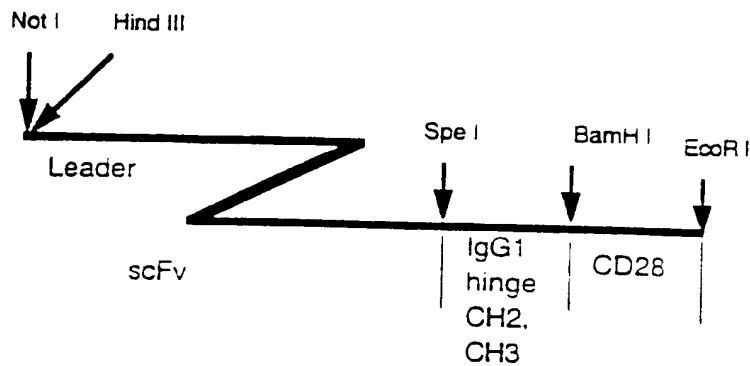
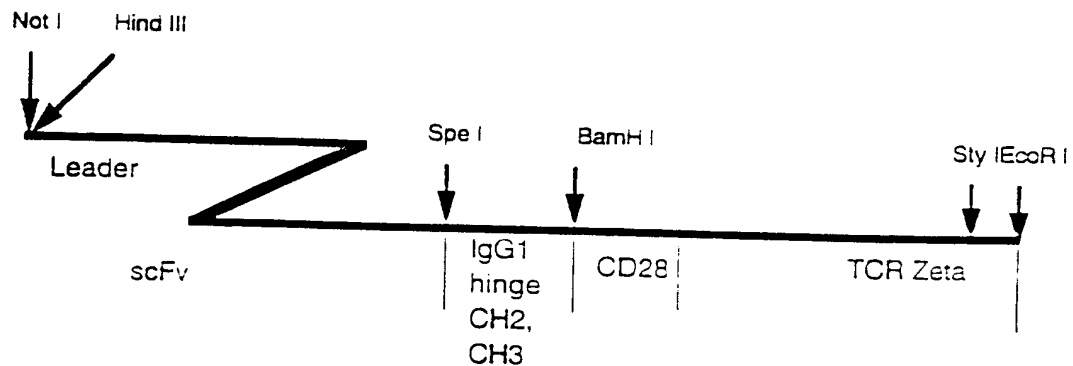
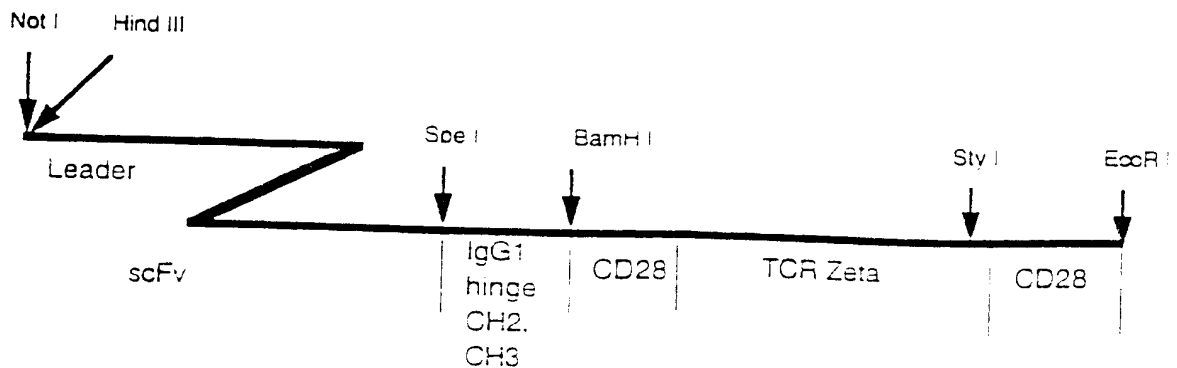
Construct cassettes cloned into pBluescript SK +

scFv / G1 / Zeta Chimeric ReceptorscFv / G1 / Zeta-CD28 fusion Chimeric ReceptorscFv / h / CD28 Chimeric Receptor

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FIG. 2b

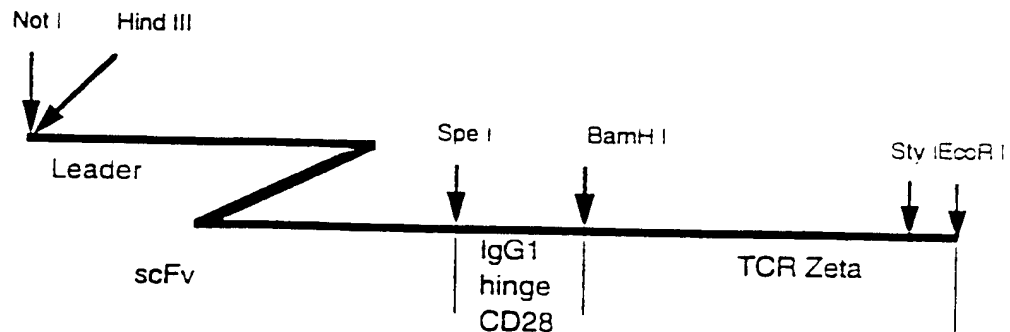
Construct cassettes cloned into pBluescript SK +

scFv /G1 /CD28 Chimeric ReceptorscFv /G1 /CD28-Zeta fusion Chimeric ReceptorscFv /G1 /CD28-Zeta-CD28 fusion Chimeric Receptor

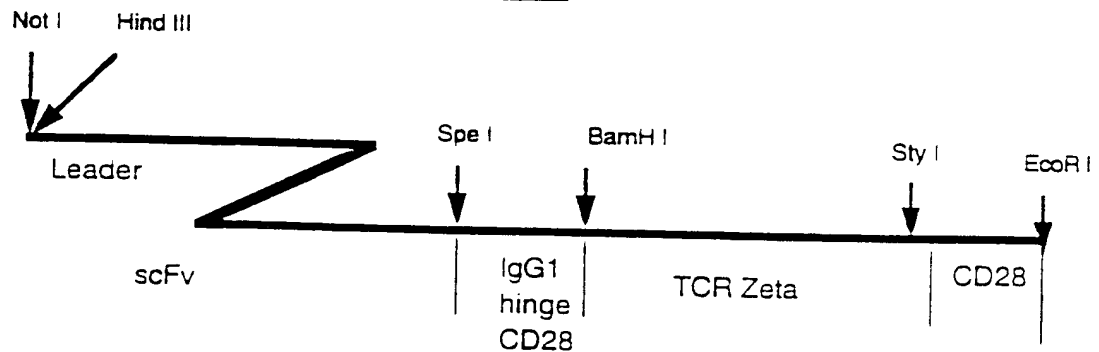
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FIG. 2c  
Construct cassettes cloned into pBluescript SK +

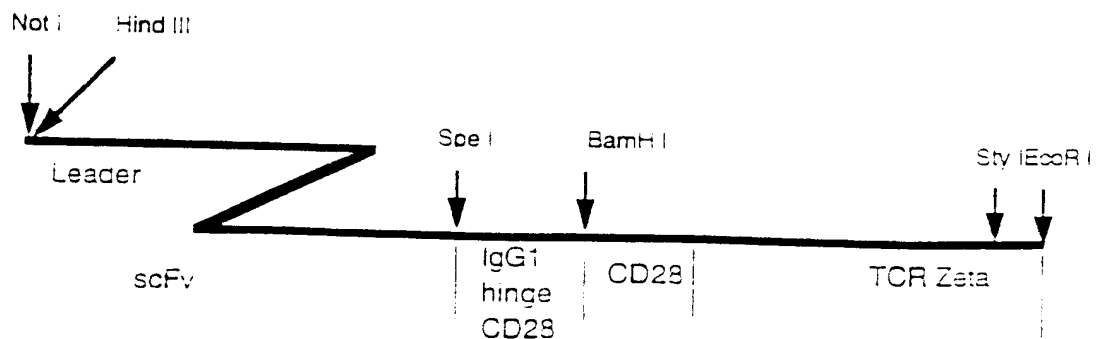
scFv / h.28 / Zeta Chimeric Receptor



scFv / h.28 / Zeta - CD28 fusion Chimeric Receptor



scFv / h.28 / CD28-Zeta fusion Chimeric Receptor



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FIG. 3  
OLIGONUCLEOTIDE SEQUENCES FOR T-BODY CONSTRUCTION

All oligos listed in the 5' to 3' orientation.

- R6490 : ATA TAG CGG CCG CAA GCT TCC ACC ATG TCT GTC CCC ACC CAA  
 GTC CTC
- R6491 : TGA CCC TCC GCC ACC TGA CCC TCC GCC ACC TGA CCC TCC GCC  
 ACC TGA CCC TCC GCC ACC TGA CCC TCC GCC ACC TTT TAC TTC TAC TTT AGT ACC
- R6492 : GGT GGC GGA GGG TCA GGT GGC GGA GGG TCA GGT GGC GGA  
 GGG TCA GGT GGC GGA GGG TCA GAG GTG CAG CTG GTG CAG TCT
- R6493 : TAT ATA CTA GTA GAA GAC ACT GTC ACC AGT
- R6516 : TGA CCC TCC GCC ACC TGA CCC TCC GCC ACC TGA CCC TCC GCC  
 ACC TGA CCC TCC GCC ACC CGT ACG TTT TAC TTC TAC TTT
- R6515 : GGT GGC GGA GGG TCA GGT GGC GGA GGG TCA GGT GGC GGA  
 GGG TCA GGT GGC GGA GGG TCA CAG ATT CAG CTG GTG CAG TCT
- R6514 : TAT ATA CTA GTC GGG CCC TTC GTT GAG GCA
- R6494 : ATA TAA CTA GTA ACT CCA TCA TGT ACT TCA GCC ACT TCG TGC  
 CGG TCT TCC TGC CAG CG
- R6495 : CGG TGT TGG TGG TCG CGG CGC TGG CGT CGT GGT GGG CTT CGC  
 TGG CAG GAA GAC CGG CAC
- R6496 : GCG CCG CGA CCA CCA ACA CCG GCG CCC ACC ATC GCG TCG CAG  
 CCC CTG TCC CTG CGC CCA
- R6497 : TAT ATG GAT CCA GCA GGC CAA AGC TCT GCG COT CTG GGC GCA  
 GGG ACA GGG GCT G
- R6506 : TAT ATG GAT CCC GCC TCT GGG CGC AGG GAC AGG GGC TG
- R6488 : ATA TAG GAT CCC AAA CTC TGC TAC CTG CTG

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## FIG. 3(contd.)

R6489 : TAT ATG AAT TCT TAG CGA GGG GGC AGG GCC TGC AT  
 P3240 : TAT GGA TCC AAG CCC TTT TGG GTG CTG GTG GTG  
 P3241 : TAT GAA TTC TCA GGA GCG ATA GGC TGC GAA  
 P3301 : GCC ACC AAG GAC ACC TAC GAC GC  
 P3302 : CCC CCT CGC AGG AGT AAG AGG AGC AGG CTC CTG CAC AGT GAC  
 TAC ATG AAC ATG ACT CCC C  
 P3303 : CAA GCA TTA CCA GCC CTA TGC CCC ACC ACG CGA CTT CGC AGC  
 CTA TCG CTC CTG AGA ATT CAT A  
 P3304 : TAT GAA TTC TCA GGA GCG ATA G  
 P3305 : GCA TAG GGCTGG TAA TGC TTG CGG GTG GGC CCG GGG CGG CGG  
 GGA GTC ATG TTC ATG TAG T  
 P3306 : CTC TTA CTC CTG CGA GGG GGC AGG GCC TGC ATG TGA AGG GCG  
 TCG TAG GTG TCC TTG GTG GC  
 S0146 : CGA CTA GTG ACA AAA CTC ACA CAT GCC CAC CGT GCC CAA AAG  
 GGA AAC ACC TTT GTC CAA GGT CCC  
 S0060 : CGA CTA GTG ACA AAA CTC ACA CAT GCC CAC CG  
 S0061 : TTG GGA TCC AGT TTA CCC GGA GAC AGG GAG AGG CT  
 T4057 : CTA CTA GTG ACA AAA CTC ACA C  
 T4058 : TTG GGA TCC AGG GGC TTA GAA GGT CCG GGA AAT AG  
 T7145 : CTG GAT CCC AAA TTT TGG GTG CTG GTG GTG GTT G  
 T4060 : GCT CCT GCT GAA CTT CAC TCT GGA GCG ATA GGC TGC GAA GTC G  
 T4387 : GCG ACT TCG CAG CCT ATC GCT CCA GAG TGA AGT TCA GCA GGA  
 GCG  
 S4700 : TAT GAA TTC TTA GCG AGG GGG CAG GGC CTG CAT G

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FIG. 4

SEQUENCE OF RCTM01 / CD8 / ZETA RECOMBINANT CHIMERIC RECEPTOR

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      10      20      30      40
      *      *      *      *
ATG TCT GTC CCC ACC CAA GTC CTC GGA CTC CTG CTG CTG TGG
TAC AGA CAG GGG TGG GTT CAG GAG COT GAG GAC GAC GAC ACC
M S V P T Q V L G L L L L W>

      50      60      70      80
      *      *      *      *
CTT ACA GAT GGC AGA TGC GAT ATC CAG ATG ACT CAG AGT CCA
GAA TGT CTA CGG TCT ACG CTA TAG GTC TAC TGA GTC TCA GGT
L T D A R C D I Q M T Q S P>

      90      100      110      120
      *      *      *      *
AGT ACT CTC AGT GGC AGT GTA GGT GAT AGG GTC ACC ATC ACT
TCA TGA GAG TCA CGG TCA CAT CCA CTA TCC CAG TGG TAG TGA
S T L S A S V G D R V T T T>

      130      140      150      160
      *      *      *      *
TGT AGG AGT AGT AAA AGT CTC CTC CAT AGT AAC GGT GAC ACC
ACA TCC TCA TCA TTT TCA GAG GAG GTA TCA TTG CCA CTG TGG
C R S S K S L L H S N G D T>

      170      180      190      200      210
      *      *      *      *      *
TTC CTC TAT TGG TTC CAG CAG AAA CCA GGT AAA GCC CCA AAG
AAG GAG ATA ACC AAG GTC GTC TTT GGT CCA TTT CGG GGT TTC
F L Y W F Q Q K P G K A P K>

      220      230      240      250
      *      *      *      *
CTC CTC ATG TAT AGG ATG AGT AAC CTC GGC AGT GGT GTA CCA
GAG GAG TAC ATA TCC TAC TCA TTG GAG CGG TCA CCA CAT GGT
L L M Y R M S N L A S G V P>

      260      270      280      290
      *      *      *      *
TCT AGA TTC AGT GGT AGT GGT AGT GGT ACT GAG TTC ACT CTC
AGA TCT AAG TCA CCA TCA CCA TCA CCA TGA CTC AAG TGA GAG
S R F S G S G S G T E F T L>

      300      310      320      330
      *      *      *      *
ACT ATC AGT AGT CTC CAG CCA GAT GAT TTC GCC ACT TAT TAT
TGA TAG TCA TCA GAG GTC GGT CTA CTA AAG CGG TGA ATA ATA
T I S S L Q P D D F A T Y Y>

      340      350      360      370
      *      *      *      *
TGT ATG CAG CAT CTC GAA TAT CCA TTC ACT TTC GGT CAG GGT
ACA TAC GTC GTA GAG CTT ATA GGT AAG TGA AAG CCA CTC CCA
C M Q H L E Y P F T F G Q G>

      380      390      400      410      420
      *      *      *      *      *
ACT AAA GTA GAA GTA AAA COT ACG GGT GGC CCA GGG TCA GGT
TGA TTT CAT CTT CAT TTT GCA TGC CCA CGG COT CCC AGT CCA
T K V E V K R T G G G G S S G>

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FIG. 4(contd.)

430 440 450 460  
 GGC GGA GGG TCA GGT GGC GGA GGG TCA GGT GGC GGA GGG TCA  
 CCG CCG CCC AGT CCA CCG CCG CCC AGT CCA CCG CCG CCC AGT  
 G G G S G G G S G G G S>

470 480 490 500  
 GGT GGC GGA GGG TCA CAG ATT CAG CTG GTG CAG TCT GGA GCA  
 CCA CCG CCG CCC AGT GTC TAA GTC GAC CAC GTC AGA CCG CCG  
 G G G G S Q I Q L V Q S G A>

510 520 530 540  
 GAG GTG AAG AAG CCG GGA TCT TCT GTG AAG GTG TCT TCT AAG  
 CTC CAC TTC TTC GGA CCG AGA AGA CAC TTC CAC AGA ACA TTC  
 E V K K P G S S V K V S C K>

550 560 570 580  
 GCA TCT GGA TAC ACC TTC ACC GAC TAC TAC ATT AAT TGG ATG  
 CGT AGA CCG ATG TGG AAG TGG CTG ATG ATG TAA TTA ACC TAC  
 A S G Y T F T D Y Y I N W M>

590 600 610 620 630  
 AGA CAG GCA CCG GGA CAG GGA CTC GAG TGG ATT GGA TGG ATT  
 TCT GTC CCG GGA CCG GTC CCG GAG CTC ACC TAA CCG ACC TAA  
 R Q A P G Q G L E W I G W I>

640 650 660 670  
 GAC CCG GGA TCT GGA AAT ACA AAG TAC AAT GAG AAG TTC AAG  
 CTG GGA CCG AGA CCG TTA TGT TTC ATG TTA CTC TTC AAG TTC  
 D P G S G N T K Y N E K F K>

680 690 700 710  
 GGA AGA GCA ACA CTG ACA GTG GAC ACA TCC ACC AAT ACC GGC  
 CCG TCT CCG TCT GAC TCT CAC CTG TGT AGG TCC TTA TGG CCG  
 G R A T L T V D T S T N T A>

720 730 740 750  
 TAC ATG GAG CTG TCT TCT CTG AGA TCT GAG GAC ACA GCA TTC  
 ATG TAC CTG GAC AGA AGA GAC TCT AGA CTC CTG TCT CCG AAG  
 Y M E L S S L R S E D T A F>

760 770 780 790  
 TAC TTC TCT GCA AGA GAG AAG ACC ACC TAC TAC TAC GCA ATG  
 ATG AAG ACA CCG TCT CTG TTC TGG TGG ATG ATG ATG CCG TAC  
 Y F C A R E H T T Y Y Y A M>

800 810 820 830 840  
 GAC TAC TGG GGA CAG GGA ACA CTG CTG AGA CTG TCT TCT GGC  
 CTG ATG ACC CCG CTG CCG TCT GAC CAG TCT CAG AGA ACA CCG  
 D Y W G Q G T L V T V C C A>



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FIG. 4(contd.)

850                      860                      870                      880  
 TCA ACG AAG GGC CCG ACT AGT AAC TCC ATC ATG TAC TTC AGC  
 AGT TGC TTC CCG GGC TGA TCA TTG AGG TAG TAC ATG AAG TCG  
 S T K G P T S N S I M Y F S>  
 890                      900                      910                      920  
 CAC TTC GTG CCG GTC TTC CTG CCA GCG AAG CCC ACC ACG ACG  
 GTG AAG CAC GGC CAG AAG GAC GGT CCG TTC GGG TGG TCG TCG  
 H F V P V F L P A K P T T T>  
 930                      940                      950                      960  
 CCA GCG CCG CGA CCA CCA ACA CCG GCG CCC ACC ATC GCG TCG  
 GGT CCC GGC GGT GGT GGT TGT GGC CCG GGG TGG TAG CCG AGC  
 P A P R P P T P A P T I A S>  
 970                      980                      990                      1000  
 CAG CCC CTG TCC CTG CCG CCA GAG GCG CAG AGC TTT GGC CTG  
 GTC GGG GAC AGG GAC GCG GGT CTC CCG GTC TCG AAA CCG GAC  
 Q P L S L R P E A Q S F G L>  
 1010                      1020                      1030                      1040                      1050  
 CTG GAT CCC AAA CTC TGC TAC CTG CTG GAT GGA ATC CTC TTC  
 GAC CTA GGG TTT GAG ACG ATG GAC GAC CTA COT TAG GAG AAG  
 L D P K L C Y L L D G I L F>  
 1060                      1070                      1080                      1090  
 ATC TAT GGT GTC ATT CTC ACT GCG TTG TTC CTG AGA GTG AAG  
 TAG ATA CCA CAG TAA GAG TGA CCG AAC AAG GAC TGT CAC TTC  
 I Y G V I L T A L F L R V K>  
 1100                      1110                      1120                      1130  
 TTC AGC AGG AGC CCA GAC GCG CCC GCG TAC CAG CAG GGC CAG  
 AAG TCG TCC TCG CGT CTC CCG GGG CCG ATG GTC GTC CCG GTC  
 F S R S A D A P A Y Q Q G Q>  
 1140                      1150                      1160                      1170  
 AAC CAG CTC TAT AAC GAG CTC AAT CTA GGA CGA AGA GAG GAG  
 TTG GTC GAG ATA TTG CTC GAG TTA GAT COT GGT TGT CTC CTC  
 N Q L Y N E L N L G R R E E>  
 1180                      1190                      1200                      1210  
 TAC GAT GTT TTG GAC AAG AGA COT GCG CCG GAC COT GAG ATG  
 ATG CTA CAA AAC CTC TTC TGT GCA CCG GCG CCG GGA CTC TAC  
 Y D V L D K R R G R D P E M>  
 1220                      1230                      1240                      1250                      1260  
 GGG GGA AAG CCG AGA AGG AAG AAC COT CAG GAA GCG CTC TAC  
 CCC COT TTC GCG TGT TCG TTC TTG GGA GTC CTT CCG GAC ATG  
 G G K P R R K N P I E D L Y>

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:

FIG. 4(contd)

1270				1280				1290				1300			
AAT	GAA	CTG	CAG	AAA	GAT	AAG	ATG	GCG	GAG	GCC	TAC	AGT	GAG		
TTA	CTT	GAC	GTC	TTT	CTA	TTC	TAC	CGC	CTC	CGG	ATG	TCA	CTC		
N	E	L	Q	K	D	K	M	A	E	A	Y	S	E>		
1310				1320				1330				1340			
ATT	GGG	ATG	AAA	GGC	GAG	CGC	CGG	AGG	GGC	AAG	GGG	CAC	GAT		
TAA	CCC	TAC	TTT	CCG	CTC	GCG	GCC	TCC	CCG	TTC	CCC	GTG	CTA		
I	G	M	K	G	E	R	R	R	G	K	G	H	D>		
1350				1360				1370				1380			
GGC	CTT	TAC	CAG	GGT	CTC	AGT	ACA	GCC	ACC	AAG	GAC	ACC	TAC		
CCG	GAA	ATG	GTC	CCA	GAG	TCA	TGT	CGG	TGG	TTC	CTG	TGG	ATG		
G	L	Y	Q	G	L	S	T	A	T	K	D	T	Y>		
1390				1400				1410				1420			
GAC	GCC	CTT	CAC	ATG	CAG	GCC	CTG	CCC	CCT	CGC	TAA				
CTG	CCG	GAA	GTG	TAC	CTC	CGG	GAC	GGG	GGA	GCG	ATT				
D	A	L	H	M	Q	A	L	P	P	R	*				

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## FIG. 5

SEQUENCE OF hCTMO1-CD8 /Zeta-CD28 FUSION RECOMBINANT  
CHIMERIC RECEPTOR

```

      10      20      30      40
      *      *      *      *
ATG TCT GTC CCC ACC CAA GTC CTC GGA CTC CTG CTG CTG TGG CTT ACA
TAC AGA CAG GGG TGG GTT CAG GAG CCT GAG GAC GAC ACC GAA TGT
m s v p t q v l g l l l l w l t>

      50      60      70      80      90
      *      *      *      *      *
GAT GCC AGA TGC GAT ATC CAG ATG ACT CAG AGT CCA AGT ACT CTC AGT
CTA CGG TCT ACG CTA TAG GTC TAC TGA GTC TCA GGT TCA TGA GAG TCA
d a f c D I Q M T Q S P S T L S>

     100     110     120     130     140
     *     *     *     *     *
GCC AGT GTA GGT GAT AGG GTC ACC ATC ACT TGT AGG AGT AGT AAA AGT
CGG TCA CAT CCA CTA TCC CAG TGG TAG TGA ACA TCC TCA TCA TTT TCA
A S V G D R V T I T C R S S K S>

     150     160     170     180     190
     *     *     *     *     *
CTC CTC CAT AGT AAC GGT GAC ACC TTC CTC TAT TGG TTC CAG CAG AAA
GAG GAG GTA TCA TTG CCA CTG TGG AAG GAG ATA ACC AAG GTC GTC TTT
L L H S N G D T F L Y W F Q Q K>

     200     210     220     230     240
     *     *     *     *     *
CCA GGT AAA GCC CCA AAG CTC CTC ATG TAT AGG ATG AGT AAC CTC GCC
GGT CCA TTT CGG GGT TTC GAG GAG TAC ATA TCC TAC TCA TTG GAG CGG
P G K A P K L L M Y R M S N L A>

     250     260     270     280
     *     *     *     *
AGT GGT GTA CCA TCT AGA TTC AGT GGT AGT GGT AGT GGT ACT GAG TTC
TCA CCA CAT GGT AGA TCT AAG TCA CCA TCA CCA TCA CCA TGA CTC AAG
S G V P S R F S G S G S G T E F>

     290     300     310     320     330
     *     *     *     *     *
ACT CTC ACT ATC AGT AGT CTC CAG CCA GAT GAT TTC GCC ACT TAT TAT
TGA GAG TGA TAG TCA TCA GAG GTC GGT CTA CTA AAG CGG TGA ATA ATA
T L T I S S L Q P D D F A T Y Y>

     340     350     360     370     380
     *     *     *     *     *
TGT ATG CAG CAT CTC GAA TAT CCA TTC ACT TTC GGT CAG GGT ACT AAA
ACA TAC GTC GTA GAG CTT ATA GGT AAG TGA AAG CCA GTC CCA TGA TTT
C M Q H L E Y P F T F G Q G T K>

     390     400     410     420     430
     *     *     *     *     *
GTA GAA GTA AAA CTT ACG GGT GGC GGA GGG TCA GGT GGC GGA GGG TCA
CAT CTT CAT TTT CCA TGC CCA CGG CTT CGG AGT CCA CGG CTT CGG AGT
V E V K R T G G G G S G S G S G S>

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## FIG. 5(contd.)

440 450 460 470 480  
 GGT GGC GGA GGG TCA GGT GGC GGA GGG TCA GGT GGC GGA GGG TCA CAG  
 CCA CCG CCT CCC AGT CCA CCG CCT CCC AGT CCA CCG CCT CCC AGT GTC  
 G G G G S G G G G S G G G G S Q>

490 500 510 520  
 ATT CAG CTG GTG CAG TCT GGA GCA GAG GTG AAG AAG CCT GGA TCT TCT  
 TAA GTC GAC CAC GTC AGA COT CGT CTC CAC TTC TTC GGA COT AGA AGA  
 I Q L V Q S G A E V K K P G S S>

530 540 550 560 570  
 GTG AAG GTG TCT TCT AAG GCA TCT GGA TAC ACC TTC ACC GAC TAC TAC  
 CAC TTC CAC AGA ACA TTC COT AGA COT ATG TGG AAG TGG CTG ATG ATG  
 V K V S C K A S G Y T F T D Y Y>

580 590 600 610 620  
 ATT AAT TGG ATG AGA CAG GCA COT GGA CAG GGA CTC GAG TGG ATT GGA  
 TAA TTA ACC TAC TCT GTC COT GGA COT GTC COT GAG CTC ACC TAA COT  
 I N W M R Q A P G Q G L E W I G>

630 640 650 660 670  
 TGG ATT GAC COT GGA TCT GGA AAT ACA AAG TAC AAT GAG AAG TTC AAG  
 ACC TAA CTG GGA COT AGA COT TTA TGT TTC ATG TTA CTC TTC AAG TTC  
 W I D P G S G N T K Y N E K F K>

680 690 700 710 720  
 GGA AGA GCA ACA CTG ACA GTG GAC ACA TCC ACC AAT ACC GGC TAC ATG  
 COT TCT COT TCT GAC TGT CAC CTG TGT AGG TGC TTA TGG CCG ATG TAC  
 G R A T L T V D T S T N T A Y M>

730 740 750 760  
 GAG CTG TCT TCT CTG AGA TCT GAG GAC ACA GCA TTC TAC TTC TGT GCA  
 CTC GAC AGA AGA GAC TCT AGA CTC CTG TGT COT AAG ATG AAG ACA COT  
 E L S S L R S E D T A F Y F C A>

770 780 790 800 810  
 AGA GAG AAG ACC ACC TAC TAC TAC GCA ATG GAC TAC TGG GGA CAG GGA  
 TCT CTC TTC TGG TGG ATG ATG ATG COT TAC CTC ATG ACC COT GTC COT  
 R E K T T Y Y Y A M D Y W G Q G>

820 830 840 850 860  
 ACA CTG GTG ACA GTG TCT TCT GGC TCA ACC AAG GGC CCG ACT ACT AAC  
 TGT GAC CAC TCT CAC AGA AGA CCG ACT TGC TTC CCG GGC TGA TCA TTC  
 T L V T V S S A S T K G P T S N>

870 880 890 900 910  
 TCC ATC ATG TAC TTC ACC CAC TTC GTC CCG GTC TTC CTG CCA GCG AAG  
 AGG TAG TAC ATG AAG TGG GTG AAG CAC GGC CAG AAG GAC GGT CCG TTC  
 S I M Y F E H F V P V F L P A K>

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## FIG. 5(contd.)

920 930 940 950 960  
 CCC ACC ACG ACG CCA GCG CCG CGA CCA CCA ACA CCG GCG CCC ACC ATC  
 GGG TGG TGC TGC GGT CGC GGC GGT GGT TGT GGC CGC GGG TGG TAG  
 P T T T P A P R P P T P A P T I>

970 980 990 1000  
 GCG TCG CAG CCC CTG TCC CTG CGC CCA GAG GCG CAG AGC TTT GGC CTG  
 CGC AGC GTC GGG GAC AGG GAC GCG GGT CTC CGC GTC TCG AAA CCG GAC  
 A S Q P L S L R P E A Q S F G L>

1010 1020 1030 1040 1050  
 CTG GAT CCC AAA CTC TGC TAC CTG CTG GAT CGA ATC CTC TTC ATC TAT  
 GAC CTA GGG TTT GAG ACG ATG GAC GAC CTA COT TAG GAG AAG TAG ATA  
 L D P K L C Y L L D G I L F I Y>

1060 1070 1080 1090 1100  
 GGT GTC ATT CTC ACT GCC TTG TTC CTG AGA GTG AAG TTC AGC AGC AGC  
 CCA CAG TAA GAG TGA CCG AAC AAG GAC TGT CAC TTC AAG TCG TCG TCG  
 G V I L T A L F L R V K F S R S>

1110 1120 1130 1140 1150  
 GCA GAC GCG CCC GCG TAC CAG CAG GCG CAG AAC CAG CTC TAT AAC GAG  
 CGT CTG CCG GGG CCG ATG GTC GTC CCG GTC TTG GTC GAG ATA TTG CTC  
 A D A P A Y Q Q G Q N Q L Y N E>

1160 1170 1180 1190 1200  
 CTC AAT CTA GGA CGA AGA GAG GAG TAC GAT GTT TTG GAC AAG AGA COT  
 GAG TTA GAT COT GGT TGT CTC CTC ATG CTA CAA AAC CTG TTC TGT GCA  
 L N L G R R E E Y D V L D K R R>

1210 1220 1230 1240  
 GGC CCG GAC COT GAG ATG GCG GGA AAG CCG AGA AGG AAG AAC COT CAG  
 CCG GCC CTG GGA CTC TAC CCG COT TTC GGC TGT TCG TTC TTG GGA GTC  
 G R D P E M G G K P R R K N P Q>

1250 1260 1270 1280 1290  
 GAA GCG CTG TAC AAT GAA CTG CAG AAA GAT AAG ATG GCG GAG GCC TAC  
 CTT CCG GAC ATG TTA CTT GAC GTC TTT CTA TTC TAC CCG CTC CCG ATG  
 E G L Y N E L Q K D K M A E A Y>

1300 1310 1320 1330 1340  
 AGT GAG ATT GGG ATG AAA GCG GAG CCG CCG AGG GCG AAG GGG CAC GAT  
 TCA CAG TAA CCG TAC TTT CCG CTC GCG GCG TCG CCG TTC CCG GTG CTA  
 S E I G M K G E R R R G K G H D>

1350 1360 1370 1380 1390  
 GCG CTT TAC CAG GGT CTC AGT ACA GCG ACC AAG GAC ACC TAC GAC GCG  
 CCG GAA ATG CTC CCA GAG TCA TGT CCG TGG TTC CTC TGG ATG CTC CCG  
 G L Y Q G L S T A T K D T Y D A>

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## FIG.5(contd.)

1400		1410		1420		1430		1440	
CTT CAC ATG CAG GCC CTG CCC COT CGC AGG AGT AAG AGG AGC AGG CTC									
GAA GTG TAC GTC CGG GAC GGG GGA GCG TCC TCA TTC TCC TCG TCC GAG									
L H M Q A L P P R R S K R S R L>									
	1450		1460		1470		1480		
	CTG CAC AGT GAC TAC ATG AAC ATG ACT CCC CGC CGC CCC GGG CCC ACC								
	GAC GTG TCA CTG ATG TAC TTG TAC TGA GGG GCG GCG GGG CCC GGG TGG								
	L H S D Y M N M T P R R P G P T>								
1490		1500		1510		1520		1530	
CGC AAG CAT TAC CAG CCC TAT GCC CCA CCA CGC GAC TTC GCA GCC TAT									
GCG TTC GTA ATG GTC GGG ATA CGG GGT GGT GCG CTG AAG CGT CGG ATA									
R K H Y Q P Y A P P R D F A A Y>									
1540									
CGC TCC TGA									
GCG AGG ACT									
R S *									

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FIG. 6

SEQUENCE OF hCTMO1/CD8 / CD28 RECOMBINANT CHIMERIC RECEPTOR

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      10      20      30      40
      *      *      *      *
ATG TCT GTC CCC ACC CAA GTC CTC GGA CTC CTG CTG CTG TGG
TAC AGA CAG GGG TGG GTT CAG GAG COT GAG GAC GAC GAC ACC
M   S   V   P   T   Q   V   L   G   L   L   L   L   W>

      50      60      70      80
      *      *      *      *
CTT ACA GAT GCC AGA TGC GAT ATC CAG ATG ACT CAG AGT CCA
GAA TGT CTA CGG TCT ACG CTA TAG GTC TAC TGA GTC TCA GGT
L   T   D   A   R   C   D   I   Q   M   T   Q   S   P>

      90      100      110      120
      *      *      *      *
AGT ACT CTC AGT GCC AGT GTA GGT GAT AGG GTC ACC ATC ACT
TCA TGA GAG TCA CGG TCA CAT CCA CTA TCC CAG TGG TAG TGA
S   T   L   S   A   S   V   G   D   R   V   T   I   T>

      130      140      150      160
      *      *      *      *
TGT AGG AGT AGT AAA AGT CTC CTC CAT AGT AAC GGT GAC ACC
ACA TCC TCA TCA TTT TCA GAG GAG GTA TCA TTG CCA CTG TGG
C   R   S   S   K   S   L   L   H   S   N   G   D   T>

      170      180      190      200      210
      *      *      *      *      *
TTC CTC TAT TGG TTC CAG CAG AAA CCA GGT AAA GCC CCA AAG
AAG GAG ATA ACC AAG GTC GTC TTT GGT CCA TTT CGG GGT TTC
F   L   Y   W   F   Q   Q   K   P   G   K   A   P   K>

      220      230      240      250
      *      *      *      *
CTC CTC ATG TAT AGG ATG AGT AAC CTC GCC AGT GGT GTA CCA
GAG GAG TAC ATA TCC TAC TCA TTG GAG CGG TCA CCA CAT GGT
L   L   M   Y   R   M   S   N   L   A   S   G   V   P>

      260      270      280      290
      *      *      *      *
TCT AGA TTC AGT GGT AGT GGT AGT GGT ACT GAG TTC ACT CTC
AGA TCT AAG TCA CCA TCA CCA TCA CCA TGA CTC AAG TGA GAG
S   R   F   S   G   S   G   S   G   T   E   F   T   L>

      300      310      320      330
      *      *      *      *
ACT ATC AGT AGT CTC CAG CCA GAT GAT TTC GCC ACT TAT TAT
TGA TAG TCA TCA GAG GTC GGT CTA CTA AAG CGG TGA ATA ATA
T   I   S   S   L   Q   P   D   D   F   A   T   Y   Y>

      340      350      360      370
      *      *      *      *
TGT ATG CAG CAT CTC GAA TAT CCA TTC ACT TTC GGT CAG GGT
ACA TAC GTC GTA GAG CTT ATA GGT AAG TGA AAG CCA GTC CCA
C   M   Q   H   L   E   Y   P   F   T   F   D   I   G>

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## FIG. 6(contd.)

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380      390      400      410      420
*      *      *      *      *
ACT AAA GTA GAA GTA AAA CCG ACG GGT GGC GGA GGG TCA GGT
TGA TTT CAT CTT CAT TTT GCA TGC CCA CCG CCG CCC AGT CCA
T   K   V   E   V   K   R   T   G   G   G   G   S   G>

      430      440      450      460
*      *      *      *
GGC GGA GGG TCA GGT GGC GGA GGG TCA GGT GGC GGA GGG TCA
CCG CCG CCC AGT CCA CCG CCG CCG AGT CCA CCG CCG CCC AGT
G   G   G   S   G   G   G   G   S   G   G   G   G   S>

      470      480      490      500
*      *      *      *
GGT GGC GGA GGG TCA CAG ATT CAG CTG GTG CAG TGT GGA GCA
CCA CCG CCG CCC AGT GTC TAA GTC GAC CAC GTC AGA CCG CCG
G   G   G   G   S   Q   I   Q   L   V   Q   S   G   A>

      510      520      530      540
*      *      *      *
GAG GTG AAG AAG CCG GGA TGT TGT GTG AAG GTG TGT TGT AAG
CTC CAC TTC TTC GGA CCG AGA AGA CAC TTC CAC AGA ACA TTC
E   V   K   K   P   G   S   S   V   K   V   S   C   K>

      550      560      570      580
*      *      *      *
GCA TGT GGA TAC ACC TTC ACC GAC TAC TAC ATT AAT TGG ATG
CGT AGA CCG ATG TGG AAG TGG CTG ATG ATG TAA TTA ACC TAC
A   S   G   Y   T   F   T   D   Y   Y   I   N   W   M>

590      600      610      620      630
*      *      *      *      *
AGA CAG GCA CCG GGA CAG GGA CTC GAG TGG ATT GGA TGG ATT
TGT GTC CCG GGA CCG GTC CCG GAG CTC ACC TAA CCG ACC TAA
R   Q   A   P   G   Q   G   L   E   W   I   G   W   I>

      640      650      660      670
*      *      *      *
GAC CCG GGA TGT GGA AAT ACA AAG TAC AAT GAG AAG TTC AAG
CTG GGA CCG AGA CCG TTA TGT TTC ATG TTA CTC TTC AAG TTC
D   P   G   S   G   N   T   K   Y   N   E   K   F   K>

      680      690      700      710
*      *      *      *
GGA AGA GCA ACA CTG ACA GTG GAC ACA TCC ACC AAT ACC GGC
CGT TGT CCG TGT GAC TGT CAC CTG TGT AGG TCC TTA TGG CCG
G   R   A   T   L   T   V   D   T   S   T   N   T   A>

      720      730      740      750
*      *      *      *
TAC ATG GAG CTG TGT TGT CTG AGA TGT GAG GAC ACA GCA TTC
ATG TAC CTC GAC AGA AGA GAC TGT AGA CTC CTG TGT CCG AAG
Y   M   E   L   S   S   L   R   S   E   D   T   A   F>

      760      770      780      790
*      *      *      *
TAC TTC TGT CCA AGA GAG AAG ACC ACC TAC TAC TAC GCA ATG
ATG AAG ACA CCG TGT CTG TTC TGG TGG ATG ATG ATG CCG TAC
Y   F   C   A   R   E   K   T   T   Y   Y   Y   A   M>

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## FIG. 6(contd.)

800 810 820 830 840  
 GAC TAC TGG GGA CAG GGA ACA CTG GTG ACA GTG TGT TGT GCC  
 CTG ATG ACC COT GTC COT TGT GAC CAC TGT CAC AGA AGA CGG  
 D Y W G Q G T L V T V S S A>  
 850 860 870 880  
 TCA ACG AAG GGC CCG ACT AGT AAC TCC ATC ATG TAC TTC AGC  
 AGT TGC TTC CCG GGC TGA TCA TTG AGG TAG TAC ATG AAG TCG  
 S T K G P T S N S I M Y F S>  
 890 900 910 920  
 CAC TTC GTG CCG GTC TTC CTG CCA GCG AAG CCG ACC ACG ACG  
 GTG AAG CAC GCG CAG AAG GAC GGT CCG TTC GGG TGG TGC TGC  
 H F V P V F L P A K P T T T  
 930 940 950 960  
 CCA GCG CCG CGA CCA CCA ACA CCG GCG CCG ACC ATC GCG TCG  
 GGT CCG GCG GGT GGT GGT TGT GCG CCG GCG TGG TAG CCG AGC  
 P A P R P P T P A P T I A S>  
 970 980 990 1000  
 CAG CCC CTG TCC CTG CCG CCA GAG GCG GGA TCC AAG CCC TTT  
 GTC GGG GAC AGG GAC GCG GGT CTG CCG CCT AGG TTC GGG AAA  
 Q P L S L R P E A G S K P F>  
 1010 1020 1030 1040 1050  
 TGG GTG CTG GTG GTG GTT GGT GGA GTC CTG GGT TGG TAT AGC  
 ACC CAC GAC CAC CAC CAA CCA CCT CAG GAC CGA ACG ATA TCG  
 W V L V V V G G V L A C Y S>  
 1060 1070 1080 1090  
 TTG CTA GTA ACA GTG GCC TTT ATT ATT TTC TGG GTG AGG AGT  
 AAC GAT CAT TGT CAC CCG AAA TAA TAA AAG ACC CAC TCC TCA  
 L L V T V A F I I F W V R S>  
 1100 1110 1120 1130  
 AAG AGG AGC AGG CTC CTG CAC AGT GAC TAC ATG AAC ATG ACT  
 TTC TCC TCG TCC GAG GAC CTG TCA CTG ATG TAC TTG TAC TGA  
 K R S R L L H S D Y M N M T>  
 1140 1150 1160 1170  
 CCC CCG CCG CCG GGG CCG ACC CCG AAG CAT TAC CAG CCC TAT  
 GGG GCG GCG GCG CCG GCG TGG GCG TTC GTA ATG GTC GGG ATA  
 P R R P G P T R K H V Q P Y>  
 1180 1190 1200 1210  
 GCG CCA CCA CCG GAC TTC GCA GCG TAT CCG TCC TGA  
 CCG GGT GGT GCG CTG AAG COT CCG ATA GCG AGG ACT  
 A P P R C F A A Y R E \*

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FIG. 7

SEQUENCE OF hCTMO1 / G1 / ZETA RECOMBINANT CHIMERIC  
RECEPTOR

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      10      20      30      40
      *      *      *      *
ATG TCT GTC CCC ACC CAA GTC CTC GGA CTC CTC CTC TGG CTT ACA
TAC AGA CAG GGG TGG GTT CAG GAG COT GAG GAC GAC GAC ACC GAA TGT
M S V P T Q V L G L L L L W L T>

50      60      70      80      90
      *      *      *      *      *
GAT GCC AGA TGC GAT ATC CAG ATG ACT CAG AGT CCA AGT ACT CTC AGT
CTA CGG TCT ACG CTA TAG GTC TAC TGA GTC TCA GGT TCA TGA GAG TCA
D A R C D I Q M T Q S P S T L S>

100      110      120      130      140
      *      *      *      *      *
GCC AGT GTA GGT GAT AGG GTC ACC ATC ACT TGT AGG AGT AGT AAA AGT
CGG TCA CAT CCA CTA TCC CAG TGG TAG TGA ACA TCC TCA TCA TTT TCA
A S V G D R V T I T C R S S K S>

150      160      170      180      190
      *      *      *      *      *
CTC CTC CAT AGT AAC GGT GAC ACC TTC CTC TAT TGG TTC CAG CAG AAA
GAG GAG GTA TCA TTG CCA CTG TGG AAG GAG ATA ACC AAG GTC GTC TTT
L L H S N G D T F L Y W F Q Q K>

200      210      220      230      240
      *      *      *      *      *
CCA GGT AAA GCC CCA AAG CTC CTC ATG TAT AGG ATG AGT AAC CTC GCC
GGT CCA TTT CGG GGT TTC GAG GAG TAC ATA TCC TAC TCA TTG GAG CGG
P G K A P K L L M Y R M S N L A>

250      260      270      280
      *      *      *      *
AGT GGT GTA CCA TCT AGA TTC AGT GGT AGT GGT AGT GGT ACT GAG TTC
TCA CCA CAT GGT AGA TCT AAG TCA CCA TCA CCA TCA CCA TGA CTC AAG
S G V P S R F S G S G S G T E F>

290      300      310      320      330
      *      *      *      *      *
ACT CTC ACT ATC AGT AGT CTC CAG CCA GAT GAT TTC GCC ACT TAT TAT
TGA GAG TGA TAG TCA TCA GAG GTC GGT CTA CTA AAG CGG TGA ATA ATA
T L T I S S L Q P D D F A T Y Y>

340      350      360      370      380
      *      *      *      *      *
TGT ATG CAG CAT CTC GAA TAT CCA TTC ACT TTC GGT CAG GGT ACT AAA
ACA TAC CTC GTA GAG CTT ATA GGT AAG TGA AAG CCA GTC CCA TGA TTT
C M Q H L E Y P F T F G Q G T K>

390      400      410      420      430
      *      *      *      *      *
GTA GAA GTA AAA COT ACG GGT GGC GGA GGG TCA GGT GGC GGA GGG TCA
CAT CTT CAT TTT CCA TCC CCA CCG COT CCG AGT CCA CCG COT CCG AGT
V E V K R T G G G G S G G G S>

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## FIG. 7 (contd.)

440	450	460	470	480
GGT GGC GGA GGG TCA GGT GGC GGA GGG TCA GGT GGC GGA GGG TCA CAG				
CCA CCG CCT CCC AGT CCA CCG CCT CCC AGT CCA CCG CCT CCC AGT CTC				
G G G G S G G G S G G G G S Q>				
490	500	510	520	
ATT CAG CTG GTG CAG TCT GGA GCA GAG GTG AAG AAG CCT GGA TCT TCT				
TAA GTC GAC CAC GTC AGA CCT CGT CTC CAC TTC TTC GGA CCT AGA AGA				
I Q L V Q S G A E V K K P G S S>				
530	540	550	560	570
GTG AAG GTG TCT TGT AAG GCA TCT GGA TAC ACC TTC ACC GAC TAC TAC				
CAC TTC CAC AGA ACA TTC CST AGA CCT ATG TGG AAG TGG CTG ATG ATG				
V K V S C K A S G Y T F T D Y Y>				
580	590	600	610	620
ATT AAT TGG ATG AGA CAG GCA CCT GGA CAG GGA CTC GAG TGG ATT GGA				
TAA TTA ACC TAC TCT GTC CGT GGA CCT GTC CCT GAG CTC ACC TAA CCT				
I N W M R Q A P G Q G L E W I G>				
630	640	650	660	670
TGG ATT GAC CCT GGA TCT GGA AAT ACA AAG TAC AAT GAG AAG TTC AAG				
ACC TAA CTG GGA CCT AGA CCT TTA TGT TTC ATG TTA CTC TTC AAG TTC				
W I D P G S G N T K Y N E K F K>				
680	690	700	710	720
GGA AGA GCA ACA CTG ACA GTG GAC ACA TCC ACC AAT ACC GGC TAC ATG				
CCT TCT CGT TGT GAC TGT CAC CTG TGT AGG TGC TTA TGG CCG ATG TAC				
G R A T L T V D T S T N T A Y M>				
730	740	750	760	
GAG CTG TCT TCT CTG AGA TCT GAG GAC ACA GCA TTC TAC TTC TGT GCA				
CTC GAC AGA AGA GAC TCT AGA CTC CTG TGT CGT AAG ATG AAG ACA CGT				
E L S S L R S E D T A F Y F C A>				
770	780	790	800	810
AGA GAG AAG ACC ACC TAC TAC TAC GCA ATG GAC TAC TGG GGA CAG GGA				
TCT CTC TTC TGG TGG ATG ATG ATG CGT TAC CTG ATG ACC CCT CTC CCT				
R E K T T Y Y Y A M D Y W G Q G>				
820	830	840	850	860
ACA CTG GTG ACA GTG TCT TCT GCG TCA ACC AAG GGC CCG ACT AGT GAC				
TGT GAC CAC TGT CAC AGA AGA CCG AGT TGC TTC CCG GGC TGA TCA CTG				
T L V T V S S A S T K G P T S D>				
870	880	890	900	910
AAA ACT CAC ACA TCC CCA CCG TCC CCA GCA CCT GAA CTC CTG GCG GGA				
TAT TGA GTG TGT ACC GGT GGC ACC GGT CST GGA CTT GAG GAC CCG CCT				
K T H T C P P C P A P E L L S G>				

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## FIG. 7 (contd.)

920	930	940	950	960
CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC				
GGC AGT CAG AAG GAG AAG GGG GGT TTT GGG TTC CTG TGG GAG TAC TAG				
P S V F L F P P K P K D T L M I>				
970	980	990	1000	
TCC CGG ACC CTT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC GAA				
AGG GCC TGG GGA CTC CAG TGT ACG CAC CAC CAC CTG CAC TCG GTG CTT				
S R T P E V T C V V V D V S H E>				
1010	1020	1030	1040	1050
GAC CTT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT				
CTG GGA CTC CAG TTC AAG TTG ACC ATG CAC CTG CCG CAC CTC CAC GTA				
D P E V K F N W Y V D G V E V H>				
1060	1070	1080	1090	1100
AAT GCC AAG ACA AAG CGG CGG GAG GAG CAG TAC AAC AGC AGC TAC CTT				
TTA CGG TTC TGT TTC GGC GCC CTC CTC CTC ATG TTG TCG TCG ATG GCA				
N A K T K P R E E Q Y N S T Y R>				
1110	1120	1130	1140	1150
GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG				
CAC CAG TCG CAG GAG TGG CAG GAC GTG GTC CTG ACC GAC TTA CCG TTC				
V V S V L T V L H Q D W L N G K>				
1160	1170	1180	1190	1200
GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG				
CTC ATG TTC ACG TTC CAG AGG TTG TTT CCG GAG GGT CCG GGG TAG CTC				
E Y K C K V S N K A L P A P I E>				
1210	1220	1230	1240	
AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CCA GAA CCA CAG GTG TAC				
TTT TGG TAG AGG TTT CCG TTT CCC GTC GGG GGT CTT GGT GTC CAC ATG				
K T I S K A K G Q P R E P Q V Y>				
1250	1260	1270	1280	1290
ACC CTG CCC CCA TCC CGG GAG GAG ATG ACC AAG AAC CAG GTC AGC CTC				
TGG GAC GGG GGT AGG GCC CTC CTC TAC TGG TTC TTG GTC CAG TCG GAC				
T L P P S R E E M T K N Q V S L>				
1300	1310	1320	1330	1340
ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC CTG GAG TGG				
TGG ACG GAC CAG TTT CCG AAG ATA GGG TCG CTC TAG CCG CAC CTC ACC				
T C L V K G F Y P S D I A V E W>				
1350	1360	1370	1380	1390
GAG AGC AAT GGG CAG CGG GAG AAC AAC TAC AAG ACC ACC CTT CCC CTG				
CTC TCG TTA CCC CTC GGC CTC TTG TTG ATG TTC TGG TCG GGA GGG CAC				
E S N G Q P E N N Y K T T P F V>				
1400	1410	1420	1430	1440
CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC CTC GAC				
GAC CTC AGG CTC CCG AGG AAG AAG GAG ATG TCG TTC GAG TGG CAC CTC				
L D S D G S F F L Y S K L T V D>				

## 21/40 FIG. 7(contd.)

1450 1460 1470 1480  
AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TGA TGC TGC GTC ATG CAT  
TTC TCG TCC ACC GTC GTC CCC TTG CAG AAG AGT ACC AGG CAC TAC GTA  
K S R W Q Q G N V F S C S V M H>

1490 1500 1510 1520 1530  
GAG GGT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG  
CTC CGA GAC GTG TTG GTG ATG TGC GTC TTC TCG GAG AGG GAC AGA GGC  
E A L H N H Y T Q K S L S L S P>

1540 1550 1560 1570 1580  
GGT AAA CTG GAT CCC AAA CTC TGC TAC CTG CTG GAT GGA ATC CTC TTC  
CCA TTT GAC CTA GGG TTT GAG ACG ATG GAC GAC CTA COT TAG GAG AAG  
G K L D P K L C Y L L D G I L F>

1590 1600 1610 1620 1630  
ATC TAT GGT GTC ATT CTC ACT GCC TTG TTC CTG AGA GTC AAG TTC AGC  
TAG ATA CCA CAG TAA GAG TGA CCG AAC AAG GAC TCT CAC TTC AAG TCG  
I Y G V I L T A L F L R V K F S>

1640 1650 1660 1670 1680  
AGG AGC GCA GAC GCC CCC GCG TAC CAG CAG GGC CAG AAC CAG CTC TAT  
TCC TCG CGT CTG CCG GGG CGC ATG GTC GTC CCG GTC TTG GTC GAG ATA  
R S A D A P A Y Q Q G Q N Q L Y>

1690 1700 1710 1720  
AAC GAG CTC AAT CTA GGA CGA AGA GAG GAG TAC GAT GTT TTG GAC AAG  
TTG CTC GAG TTA GAT COT GCT TCT CTC CTC ATG CTA CAA AAC CTG TTC  
N E L N L G R R E E Y D V L D K>

1730 1740 1750 1760 1770  
AGA COT GCC CCG GAC COT GAG ATG GGG GGA AAG CCG AGA AGG AAG AAC  
TOT GCA CCG GCC CTG GGA CTC TAC CCC COT TTC GGC TOT TCC TTC TTG  
R R G R D P E M G G K P R R K N>

1780 1790 1800 1810 1820  
COT CAG GAA GGC CTG TAC AAT GAA CTG CAG AAA GAT AAG ATG GCG GAG  
GGA GTC CTT CCG GAC ATG TTA CTT GAC GTC TTT CTA TTC TAC CCG CTC  
P Q E G L Y N E L Q K D K M A E>

1830 1840 1850 1860 1870  
GCC TAC AGT GAG ATT GGG ATG AAA GGC GAG CCG CCG AGG GGC AAG GGC  
CGG ATG TGA CTC TAA CCC TAC TTT CCG CTC GCG GCG TCC CCG TTC CCC  
A Y S E I G M K G E R R R G K G>

1880 1890 1900 1910 1920  
CAC GAT GGC CTT TAC CAG GGT CTC AGT ACA GGC ACC AAG GAC ACC TAC  
GTG CTA CCG GAA ATG CTC CCA GAG TGA TOT CCG TCG TTC CTG TCG ATG  
H D G L Y Q G L S T A T K D T Y>

1930 1940 1950  
GAC GGC CTT CAC ATG CAG GGC CTG GGC COT CCG TAA  
CTG CCG GAA GTG TAC CTC CCG GAC GCG GGA GCG ATT  
D A L H M Q A L P P R >

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FIG. 8  
SEQUENCE OF hCTMO1/G1/ZETA-CD28 FUSION RECOMBINANT  
CHIMERIC RECEPTOR

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      10      20      30      40
      *      *      *      *
ATG TCT GTC CCC ACC CAA GTC CTC GGA CTC CTG CTG CTG TGG CTT ACA
TAC AGA CAG GGG TGG GTT CAG GAG CCT GAG GAC GAC GAC ACC GAA TGT
M   S   V   P   T   Q   V   L   G   L   L   L   L   W   L   T>

50      60      70      80      90
      *      *      *      *      *
GAT GGC AGA TGC GAT ATC CAG ATG ACT CAG AGT CCA AGT ACT CTC AGT
CTA CGG TCT ACG CTA TAG GTC TAC TGA GTC TCA GGT TCA TGA GAG TCA
D   A   R   C   D   I   Q   M   T   Q   S   P   S   T   L   S>

100     110     120     130     140
      *      *      *      *      *
GCC AGT GTA GGT GAT AGG GTC ACC ATC ACT TGT AGG AGT AGT AAA AGT
CGG TCA CAT CCA CTA TCC CAG TGG TAG TGA ACA TCC TCA TCA TTT TCA
A   S   V   G   D   R   V   T   I   T   C   R   S   S   K   S>

150     160     170     180     190
      *      *      *      *      *
CTC CTC CAT AGT AAC GGT GAC ACC TTC CTC TAT TGG TTC CAG CAG AAA
GAG GAG GTA TCA TTG CCA CTG AAG GAG ATA ACC AAG GTC GTC TTT
L   L   H   S   N   G   D   T   F   L   Y   W   F   Q   Q   K>

200     210     220     230     240
      *      *      *      *      *
CCA GGT AAA GCC CCA AAG CTC CTC ATG TAT AGG ATG AGT AAC CTC GCC
GGT CCA TTT CCG GGT TTC GAG GAG TAC ATA TCC TAC TCA TTG GAG CCG
P   G   K   A   P   K   L   L   M   Y   R   M   S   N   L   A>

250     260     270     280
      *      *      *      *
AGT GGT GTA CCA TCT AGA TTC AGT GGT AGT GGT AGT GGT ACT GAG TTC
TCA CCA CAT GGT AGA TCT AAG TCA CCA TCA CCA TCA CCA TGA CTC AAG
S   G   V   P   S   R   F   S   G   S   G   S   G   T   E   F>

290     300     310     320     330
      *      *      *      *      *
ACT CTC ACT ATC AGT AGT CTC CAG CCA GAT GAT TTC GGC ACT TAT TAT
TGA GAG TGA TAG TCA TCA GAG GTC GGT CTA CTA AAG CCG TGA ATA ATA
T   L   T   I   S   S   L   Q   P   D   D   F   A   T   Y   Y>

340     350     360     370     380
      *      *      *      *      *
TGT ATG CAG CAT CTC GAA TAT CCA TTC ACT TTC GGT CAG GGT ACT AAA
ACA TAC CTC GTA GAG CTT ATA GGT AAG TGA AAG CCA GTC CCA TGA TTT
C   M   Q   H   L   E   Y   P   F   T   F   G   Q   G   T   K>

390     400     410     420     430
      *      *      *      *      *
GTA GAA GTA AAA CCT ACC GGT CCG GGA GGG TCA GGT CCG GGA CCG TCA
CAT CTT CAT TTT GCA TCC CCA CCG CCT CCG AGT CCA CCG CCG CCG AGT
V   E   V   K   R   T   G   G   G   G   S   G   G   G   G   S>

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## FIG. 8(contd.)

440 450 460 470 480  
 GGT GGC GGA GGG TCA GGT GGC GGA GGG TCA GGT GGC GGA GGG TCA CAG  
 CCA CCG CCG CCC AGT CCA CCG CCG CCC AGT CCA CCG CCG CCC AGT GTC  
 G G G G S G G G S G G G G S Q>  
 490 500 510 520  
 ATT CAG CTG GTG CAG TCT GGA GCA GAG GTG AAG AAG CCG GGA TCT TCT  
 TAA GTC GAC CAC GTC AGA CCG CGT CTC CAC TTC TTC GGA CCG AGA AGA  
 I Q L V Q S G A E V K K P G S S>  
 530 540 550 560 570  
 GTG AAG GTG TCT TGT AAG GCA TCT GGA TAC ACC TTC ACC GAC TAC TAC  
 CAC TTC CAC AGA ACA TTC CGT AGA CCG ATG TGG AAG TGG CTG ATG ATG  
 V K V S C K A J G Y T F T D Y Y>  
 580 590 600 610 620  
 ATT AAT TGG ATG AGA CAG GCA CCG GGA CAG GGA CTC GAG TGG ATT GGA  
 TAA TTA ACC TAC TCT GTC CGT GGA CCG GTC CCG GAG CTC ACC TAA CCG  
 I N W M R Q A P G Q G L E W I G>  
 630 640 650 660 670  
 TGG ATT GAC CCG GGA TCT GGA AAT ACA AAG TAC AAT GAG AAG TTC AAG  
 ACC TAA CTG GGA CCG AGA CCG TTA TGT TTC ATG TTA CTC TTC AAG TTC  
 W I D P G S G N T K Y N E K F K>  
 680 690 700 710 720  
 GGA AGA GCA ACA CTG ACA GTG GAC ACA TCC ACG AAT ACC GCG TAC ATG  
 CCG TCT CCG TCT GAC TGT CAC CTG TGT AGG TGG TTA TGG CCG ATG TAC  
 G R A T L T V D T S T N T A Y M>  
 730 740 750 760  
 GAG CTG TCT TCT CTG AGA TCT GAG GAC ACA GCA TTC TAC TTC TGT GCA  
 CTC GAC AGA AGA GAC TCT AGA CTC CTG TGT CCG AAG ATG AAG ACA CCG  
 E L S S L R S E D T A F Y F C A>  
 770 780 790 800 810  
 AGA GAG AAG ACC ACC TAC TAC TAC GCA ATG GAC TAC TGG GGA CAG GGA  
 TCT CTC TTC TGG TGG ATG ATG ATG CCG TAC CTG ATG ACC CCG GTC CCG  
 R E K T T Y Y Y A M D Y W G Q G>  
 820 830 840 850 860  
 ACA CTG GTG ACA GTG TCT TCT CCG TCA ACG AAG GGC CCG ACT AGT GAC  
 TGT GAC CAC TCT CAC AGA AGA CCG AGT TGC TTC CCG GGC TGA TCA CTG  
 T L V T V S S A S T K G P T S D>  
 870 880 890 900 910  
 AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCG GAA CTC CTC GCG GGA  
 TTT TGA GTG TGT ACG GGT CCG ACG GGT CCG GGA CTT GAG GAC CCG CCG  
 K T H T C P P C P A P E L L S G>

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FIG. 8(contd.)

920	930	940	950	960
CCG TCA GTC TTC CTC TTC CCG CCA AAA CCG AAG GAC ACC CTC ATG ATC				
GGC AGT CAG AAG GAG AAG GGG GGT TTT GGG TTC CTG TGG GAG TAC TAG				
P S V F L F P P K P K D T L M Y>				
970	980	990	1000	
TCC CCG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC GAA				
AGG GCC TGG GGA CTC CAG TGT ACG CAC CAC CAC CTG CAC TCG GTG CTT				
S R T P E V T C V V V D V S H E>				
1010	1020	1030	1040	1050
GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT				
CTG GGA CTC CAG TTC AAG TTG ACC ATG CAC CTG CCG CAC CTC CAC GTA				
D P E V K F N W Y V D G V E Y H>				
1060	1070	1080	1090	1100
AAT GCC AAG ACA AAG CCG CCG GAG GAG CAG TAC AAC ACC ACC TAC CGT				
TTA CCG TTC TGT TTC GGC GCC CTC CTC GTC ATG TTG TCG TGC ATG GCA				
N A K T K P R E E Q Y N S T Y R>				
1110	1120	1130	1140	1150
GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GCC AAG				
CAC CAG TCG CAG GAG TGG CAG GAC GTG GTC CTG ACC GAC TTA CCG TTC				
V V S V L T V L H Q D W L N G K>				
1160	1170	1180	1190	1200
GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC CCG ATC GAG				
CTC ATG TTC ACG TTC CAG AGG TTG TTT CCG GAG GGT CCG GGG TAG CTC				
E Y K C K V S N K A L P A P I E>				
1210	1220	1230	1240	
AAA ACC ATC TCC AAA GCC AAA GGG CAG CCG CCA GAA CCA CAG GTG TAC				
TTT TGG TAG AGG TTT CCG TTT CCG GTC GGG GGT CTT GGT CTC CAC ATG				
K T I S K A K G Q P R E P Q V Y>				
1250	1260	1270	1280	1290
ACC CTG CCG CCA TCC CCG GAG GAG ATG ACC AAG AAC CAG GTG AGC CTG				
TGG GAC GGG GGT AGG GCC CTC CTC TAC TGG TTC TTG GTC CAG TCG GAC				
T L P P S R E E M T K N Q V S L>				
1300	1310	1320	1330	1340
ACC TGC CTG GTC AAA GGC TTC TAT CCG AGC GAC ATC CCG GTG GAG TGG				
TGG ACC GAC CAG TTT CCG AAG ATA GGG TCG CTG TAG CCG CAC CTC ACC				
T C L V K D F Y P S D I A V E W>				
1350	1360	1370	1380	1390
GAG ACC AAT GGG CAG CCG GAG AAG AAC TAC AAG ACC ACG CTT CCG GTG				
CTC TCG TTA CCG CTC GGC CTC TTG TTG ATG TTC TGG TCG GGA GGG CAC				
E S N G Q P E N N Y K T T P P V>				
1400	1410	1420	1430	1440
CTG GAC TCG GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG GAC				
GAC CTC AGG CTC CCG AGG AAG AAG GAG ATG TCG TTC GAG TGG CAC CTC				
L C S D G S F F L Y S K L T V D>				



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FIG. 8(contd.)

1450 1460 1470 1480  
 AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT  
 TTC TCG TCC ACC GTC GTC CCC TTG CAG AAG AGT ACG AGG CAC TAC GTA  
 K S R W Q Q G N V F S C S V M H>

1490 1500 1510 1520 1530  
 GAG GGT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCC  
 CTC CGA GAC GTG TTG GTG ATG TGC GTC TTC TCG GAG AGG GAC AGA GGC  
 E A L H N H Y T Q K S L S L S P>

1540 1550 1560 1570 1580  
 GGT AAA CTG GAT CCC AAA CTC TGC TAC CTG CTG GAT GGA ATC CTC TTC  
 CCA TTT GAC CTA GGG TTT GAG ACG ATG GAC GAC CTA COT TAG GAG AAG  
 G K L D P K L C Y L L D G I L F>

1590 1600 1610 1620 1630  
 ATC TAT GGT GTC ATT CTC ACT GCC TTG TTC CTG AGA GTG AAG TTC AGC  
 TAG ATA CCA CAG TAA GAG TGA CCG AAC AAG GAC TCT CAC TTC AAG TCG  
 I Y G V I L T A L F L R V K F S>

1640 1650 1660 1670 1680  
 AGG AGC GCA GAC GCC CCC GCG TAC CAG CAG GGC CAG AAC CAG CTC TAT  
 TCC TCG CGT CTG CCG GGG CGC ATG GTC GTC CCG GTC TTG GTC GAG ATA  
 R S A D A P A Y Q Q G Q N Q L Y>

1690 1700 1710 1720  
 AAC GAG CTC AAT CTA GGA CGA AGA GAG GAG TAC GAT GTT TTG GAC AAG  
 TTG CTC GAG TTA GAT COT GGT TOT CTC CTC ATG CTA CAA AAC CTC TTC  
 N E L N L G R R E E Y D V L D K>

1730 1740 1750 1760 1770  
 AGA COT GGC CCG GAC COT GAG ATG GGG GGA AAG CCC AGA AGG AAG AAC  
 TCT GCA CCG GCC CTG GGA CTC TAC CCC COT TTC GGC TCT TCC TTC TTG  
 R R G R D P E M G G K P R R K N>

1780 1790 1800 1810 1820  
 COT CAG GAA GGC CTG TAC AAT GAA CTG CAG AAA GAT AAG ATG GCG GAG  
 GGA GTC CTT CCG GAC ATG TTA CTT GAC GTC TTT CTA TTC TAC CCG CTC  
 P Q E G L Y N E L Q K D K M A E>

1830 1840 1850 1860 1870  
 GCC TAC AGT GAG ATT GGG ATG AAA GGC GAG CCC CCG AGG GGC AAG GGC  
 CCG ATG TCA CTC TAA CCC TAC TTT CCG CTC GCG CCG TCC CCG TTC CCC  
 A Y S E I G M K G E R R R G K G>

1880 1890 1900 1910 1920  
 CAC GAT GGC CTT TAC CAG GGT CTC AGT ACA GGC ACC AAG GAC ACC TAC  
 GTC CTA CCG GAA ATG CTC CCA GAG TCA TOT CCG TGG TTC CTC TGG ATG  
 H D S L Y I E L E T A T K C T Y>

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		1930		1940		1950		1960	
		GAC	GCC	CTT	CAC	ATG	CAG	GCC	CTG
		CTG	CGG	GAA	GTG	TAC	GTC	CGG	GAC
		D	A	L	H	M	Q	A	L
								P	P
								R	R
								S	K
								R	S>
1970			1980		1990		2000		2010
		AGG	CTC	CTG	CAC	AGT	GAC	TAC	ATG
		TCC	GAG	GAC	GTG	TCA	CTG	ATG	TAC
		R	L	L	H	S	D	Y	M
								N	M
								T	P
								R	R
								P	G>
		2020		2030		2040		2050	
		CCC	ACC	CGC	AAG	CAT	TAC	CAG	CCC
		GGG	TGG	GCG	TTG	GTA	ATG	GTC	GGG
		P	T	R	K	H	Y	Q	P
									Y
									A
									P
									R
									D
									F
									A>
		2070							
		GCC	TAT	CGC	TCC	TGA			
		CGG	ATA	GCG	AGG	ACT			
		A	Y	R	S	*			

FIG. 8 (contd.)

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## FIG. 9

SEQUENCE OF hCTMO1 / h CD28 RECOMBINANT CHIMERIC  
RECEPTOR

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      10      20      30      40
      *      *      *      *
ATG TGT GTC CCC ACC CAA GTC CTC GGA CTC CTG CTG CTG TGG CTT ACA
TAC AGA CAG GGG TGG GTT CAG GAG CCT GAG GAC GAC GAC ACC GAA TGT
M S V P T Q V L G L L L L W L T>

50      60      70      80      90
      *      *      *      *      *
GAT GGC AGA TGC GAT ATC CAG ATG ACT CAG AGT CCA AGT ACT CTC AGT
CTA CGG TGT ACG CTA TAG CTC TAC TGA CTC TCA GGT TCA TGA GAG TCA
D A R C D I Q M T C C P C T L D>

100     110     120     130     140
      *      *      *      *      *
GCC AGT GTA GGT GAT AGG GTC ACC ATC ACT TGT AGG AGT AGT AAA AGT
CGG TCA CAT CCA CTA TCC CAG TGG TAG TGA ACA TCC TCA TCA TTT TCA
A S V G D R V T I T C R S S K S>

150     160     170     180     190
      *      *      *      *      *
CTC CTC CAT AGT AAC GGT GAC ACC TTC CTC TAT TGG TTC CAG CAG AAA
GAG GAG GTA TCA TTG CCA CTG TGG AAG GAG ATA ACC AAG GTC GTC TTT
L L H S N G D T F L Y W F Q Q K>

200     210     220     230     240
      *      *      *      *      *
CCA GGT AAA GCC CCA AAG CTC CTC ATG TAT AGG ATG AGT AAC CTC GCC
GGT CCA TTT CGG GGT TTC GAG GAG TAC ATA TCC TAC TCA TTG GAG CGG
P G K A P K L L M Y R M C N L A>

250     260     270     280
      *      *      *      *
AGT GGT GTA CCA TGT AGA TTC AGT GGT AGT GGT AGT GGT AGT GAG TTC
TCA CCA CAT GGT AGA TGT AAG TCA CCA TCA CCA TCA CCA TGA CTC AAG
S G V P S R F S G S G S G T E F>

290     300     310     320     330
      *      *      *      *      *
ACT CTC ACT ATC AGT AGT CTC CAG CCA GAT GAT TTC GCC ACT TAT TAT
TGA GAG TGA TAG TCA TCA GAG CTC GGT CTA CTA AAG CGG TGA ATA ATA
T L T I S S L Q P D D F A T Y Y>

340     350     360     370     380
      *      *      *      *      *
TGT ATG CAG CAT CTC GAA TAT CCA TTC ACT TTC GGT CAG GGT ACT AAA
ACA TAC CTC GTA GAG CTT ATA GGT AAG TGA AAG CCA CTC CCA TGA TTT
C M Q H L E Y P F T F G Q G T K>

390     400     410     420     430
      *      *      *      *      *
GTA GAA GTA AAA COT ACG GGT GGC GGA GGG TCA GGT GGC GGA GGG TCA
CAT CTT CAT TTT CCA TCC CCA CCG COT CCG AGT CCA CCG COT CCG AGT
V E V K R T G G G G L G G G G S>

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FIG. 9 (contd.)

440 450 460 470 480  
 GGT GGC GGA GGG TCA GGT GGC GGA GGG TCA GGT GGC GGA GGG TCA CAG  
 CCA CCG CCT CCC AGT CCA CCG CCT CCC AGT CCA CCG CCT CCC AGT GTC  
 G G G G S G G G G S G G G G S Q>

490 500 510 520  
 ATT CAG CTG GTG CAG TCT GGA GCA GAG GTG AAG AAG COT GGA TCT TCT  
 TAA GTC GAC CAC CTC AGA COT CGT CTC CAC TTC TTC GGA COT AGA AGA  
 I Q L V Q S G A E V K K P G S S>

530 540 550 560 570  
 GTG AAG GTG TCT TGT AAG GCA TCT GGA TAC ACC TTC ACC GAC TAC TAC  
 CAC TTC CAC AGA ACA TTC COT AGA COT ATG TGG AAG TGG CTG ATG ATG  
 V K V C C K A S G Y T F T D Y Y>

580 590 600 610 620  
 ATT AAT TGG ATG AGA CAG GCA COT GGA CAG GGA CTC GAG TGG ATT GGA  
 TAA TTA ACC TAC TCT GTC COT GGA COT GTC COT GAG CTC ACC TAA COT  
 I N W M R Q A P G Q G L E W I G>

630 640 650 660 670  
 TGG ATT GAC COT GGA TCT GGA AAT ACA AAG TAC AAT GAG AAG TTC AAG  
 ACC TAA CTG GGA COT AGA COT TTA TGT TTC ATG TTA CTC TTC AAG TTC  
 W I D P G S G N T K Y N E K F K>

680 690 700 710 720  
 GGA AGA GCA ACA CTG ACA GTG GAC ACA TCG ACC AAT ACC GGC TAC ATG  
 COT TCT COT TGT GAC TGT CAC CTG TGT AGG TCG TTA TCG CCG ATG TAC  
 G R A T L T V D T S T N T A Y M>

730 740 750 760  
 GAG CTG TCT TCT CTG AGA TCT GAG GAC ACA GCA TTC TAC TTC TGT GCA  
 CTC GAC AGA AGA GAC TCT AGA CTC CTG TGT COT AAG ATG AAG ACA COT  
 E L S S L R S E D T A F Y F C A>

770 780 790 800 810  
 AGA GAG AAG ACC ACC TAC TAC TAC GCA ATG GAC TAC TGG GGA CAG GGA  
 TCT CTC TTC TGG TGG ATG ATG ATG COT TAC CTC ATG ACC COT CTC COT  
 R E K T T Y Y Y A M D Y W G L G>

820 830 840 850 860  
 ACA CTG GTG ACA CTG TCT TCT GGC TCA ACC AAG GGC CCG ACT ACT GAC  
 TGT GAC CAC TGT CAC AGA AGA CCG ACT TCG TTC CCG GGC TGA TGA CTG  
 T L V T V S S A S T K D P T S D>

870 880 890 900 910  
 AAA ACT CAC ACA TCG CCA CCG TCG CCA AAA GGC AAA CAC CTT TCT CCA  
 TTT TCA CTG TGT ACC GGT CCG ACC GGT TTT CCG TTT GTG GAA ACA GGT  
 K T H T C P P C P K G K H L C P>

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          920          930          940          950          960
          *          *          *          *          *
AGT CCC CTA TTT CCC GGA CCT TCT AAG CCC TTT TGG GTG CTG GTG GTG
TCA GGG GAT AAA GGG CTT GGA AGA TTC GGG AAA ACC CAC GAC CAC CAC
S   P   L   F   P   G   P   S   K   P   F   W   V   L   V   V>

          970          980          990          1000
          *          *          *          *
GTT GGT GGA GTC CTG GCT TGC TAT AGC TTG CTA GTA ACA GTG GCC TTT
CAA CCA CCT CAG GAC CGA ACG ATA TCG AAC GAT CAT TGT CAC CGG AAA
V   G   G   V   L   A   C   Y   S   L   L   V   T   V   A   F>

1010          1020          1030          1040          1050
*          *          *          *          *
ATT ATT TTC TGG GTG AGG AST AAG AGG AGC AGG CTC CTG CAC AST GAC
TAA TAA AAG ACC CAC TCC TCA TTC TCC TCC TCC GAG GAC GTG TCA CTG
I   I   F   W   V   R   S   K   R   S   R   L   L   H   S   D>

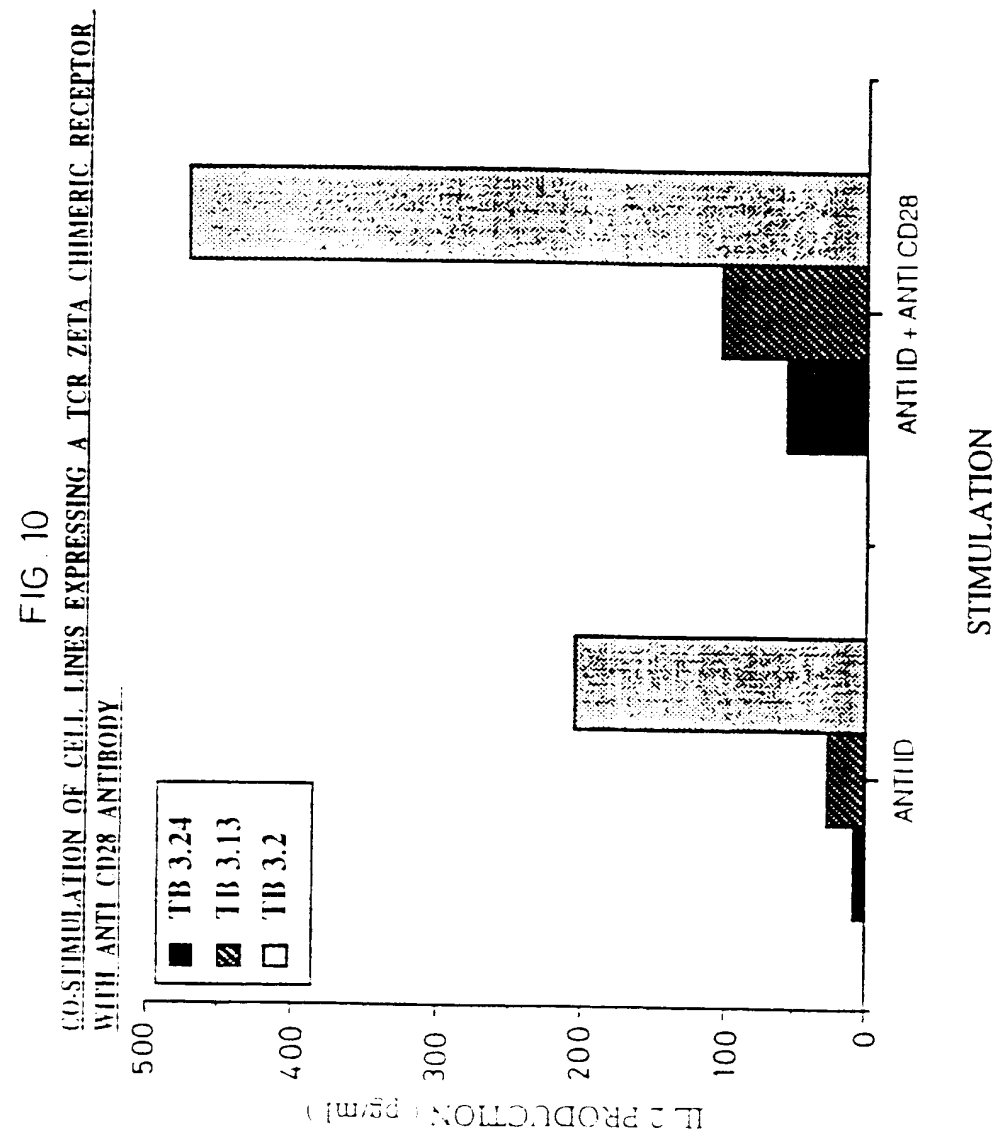
1060          1070          1080          1090          1100
          *          *          *          *          *
TAC ATG AAC ATG ACT CCC CGC CGC CCC GGG CCC ACC CGC AAG CAT TAC
ATG TAC TTG TAC TGA GGG GCG GCG GGG CCC GGG TGG GCG TTC GTA ATG
Y   M   N   M   T   P   R   R   P   G   P   T   R   K   H   Y>

1110          1120          1130          1140
          *          *          *          *
CAG CCC TAT GCC CCA CCA CGC GAC TTC GCA GCC TAT CGC TCC TGA
GTC GGG ATA CGG GGT GGT GCG CTG AAG CGT CGG ATA GCG AGG ACT
Q   P   Y   A   P   P   R   D   F   A   A   Y   R   S   *

```

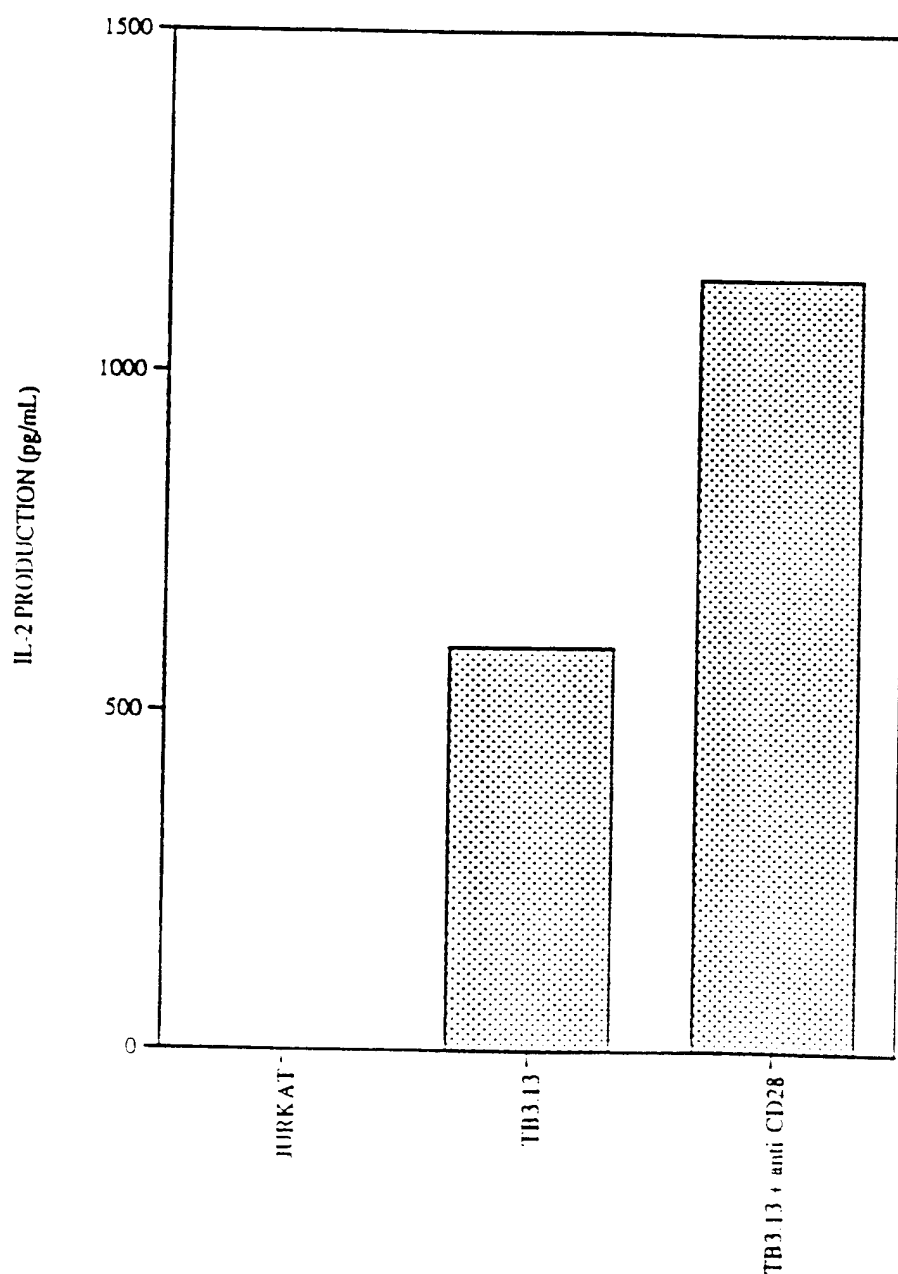
FIG. 9(contd.)

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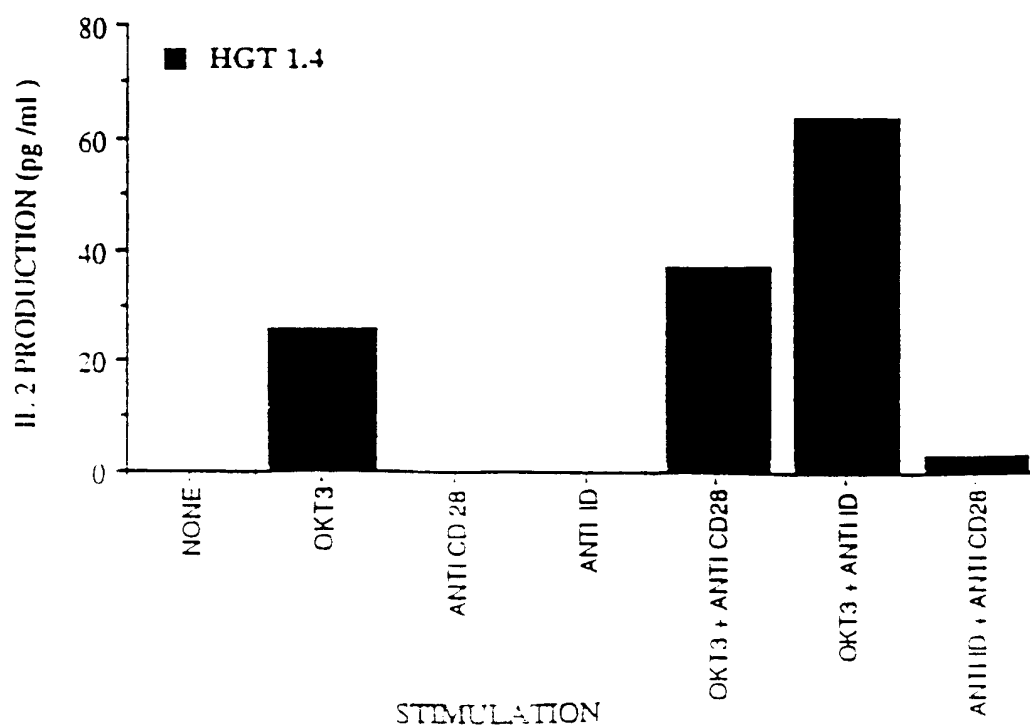
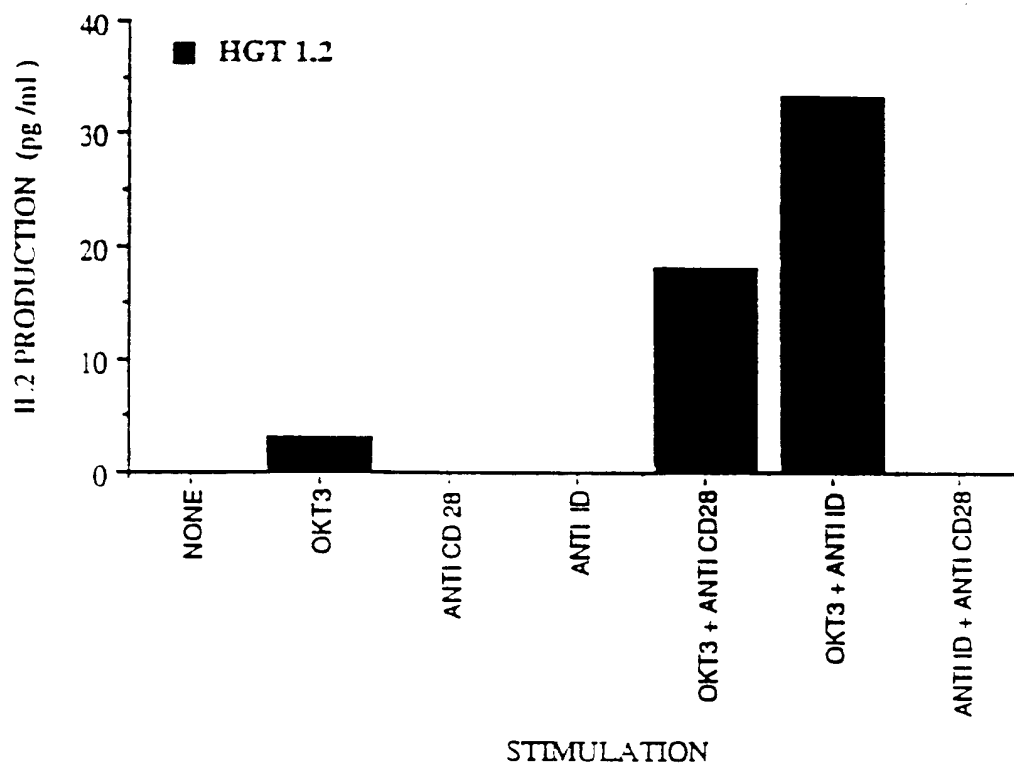
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FIG. 11  
STIMULATION WITH ANTIGEN POSITIVE CELLS.MCF-7



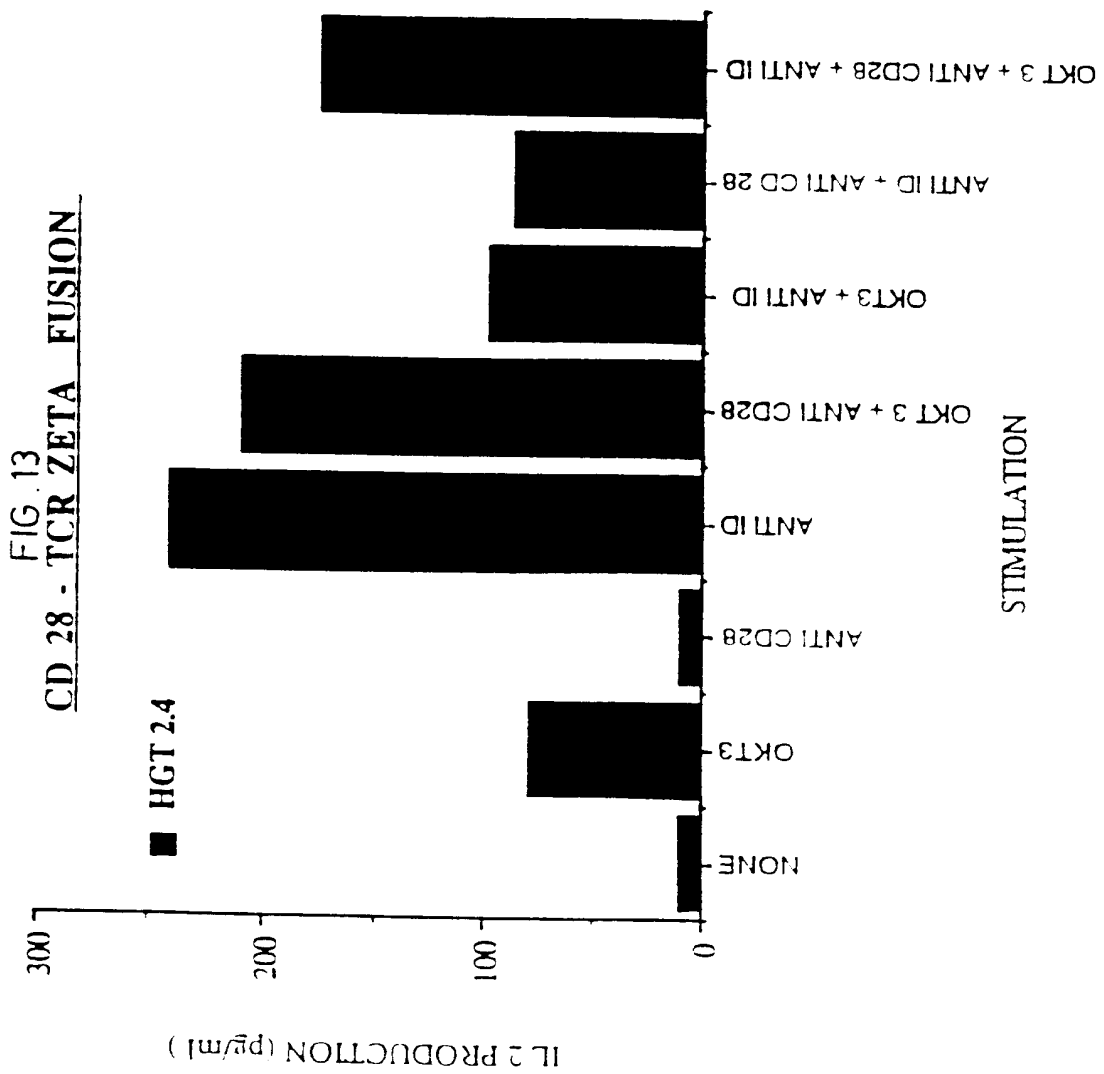
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FIG. 12

IL2 PRODUCTION IN RESPONSE TO VARIOUS STIMULI

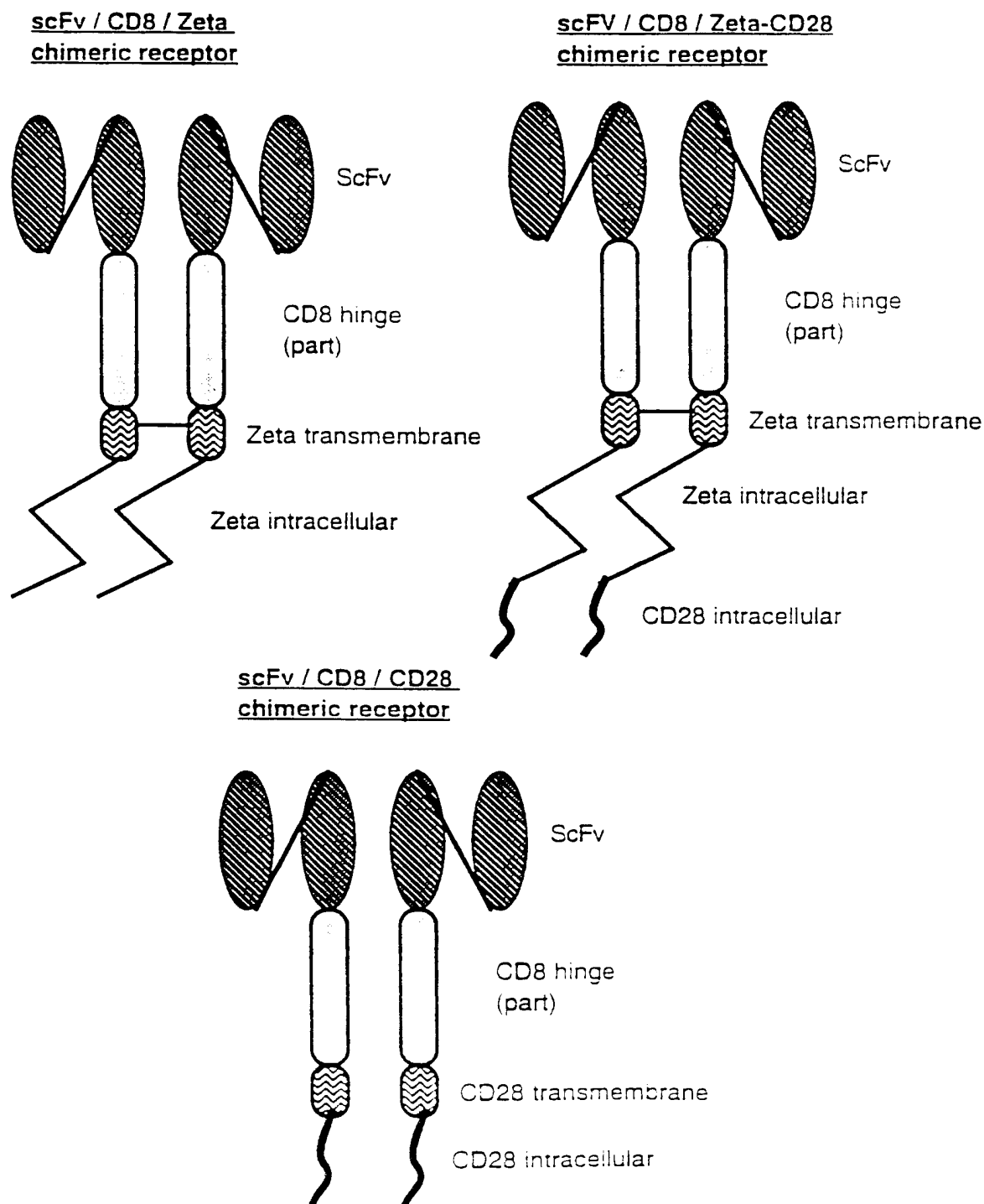


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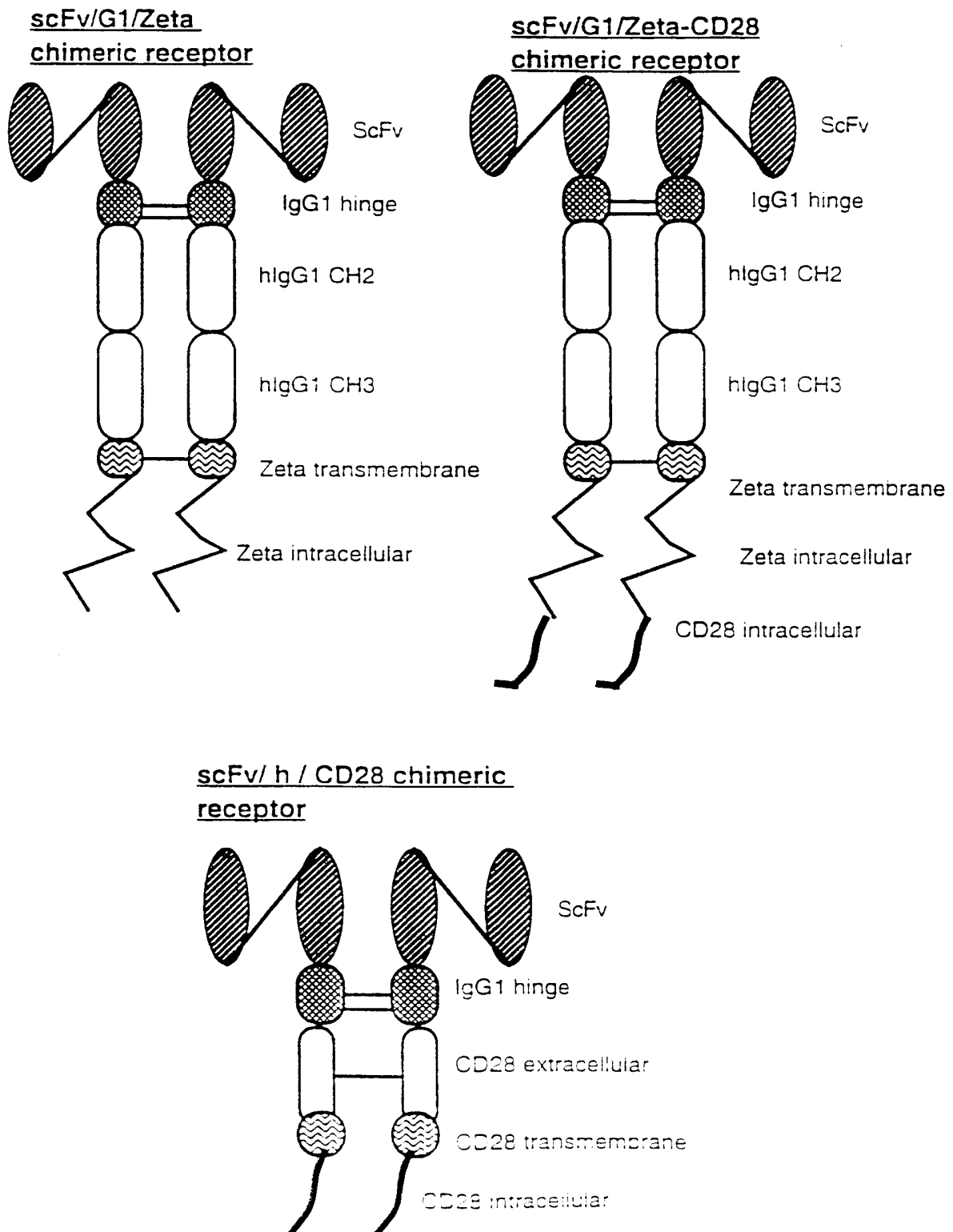
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FIG. 14



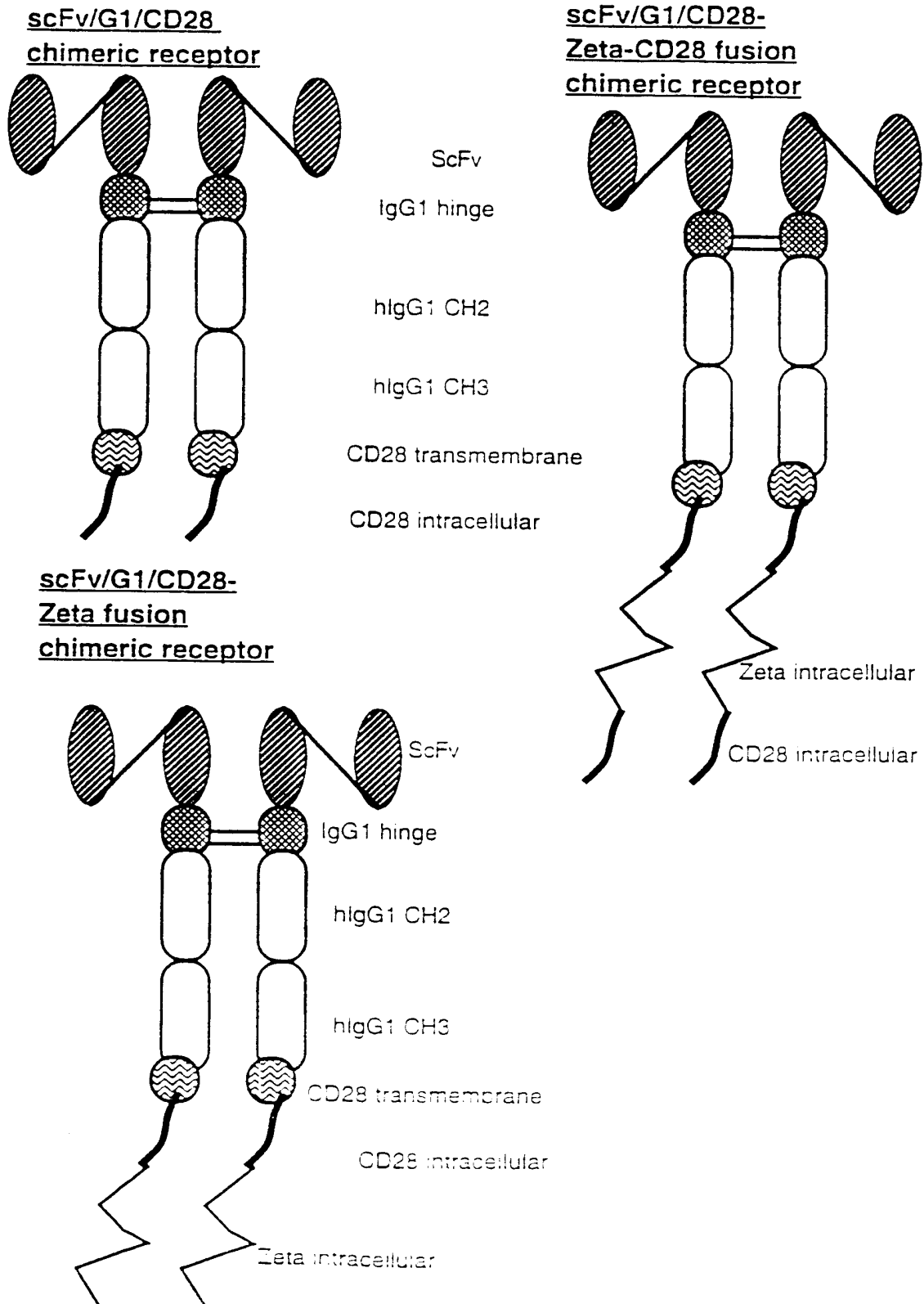
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FIG. 15



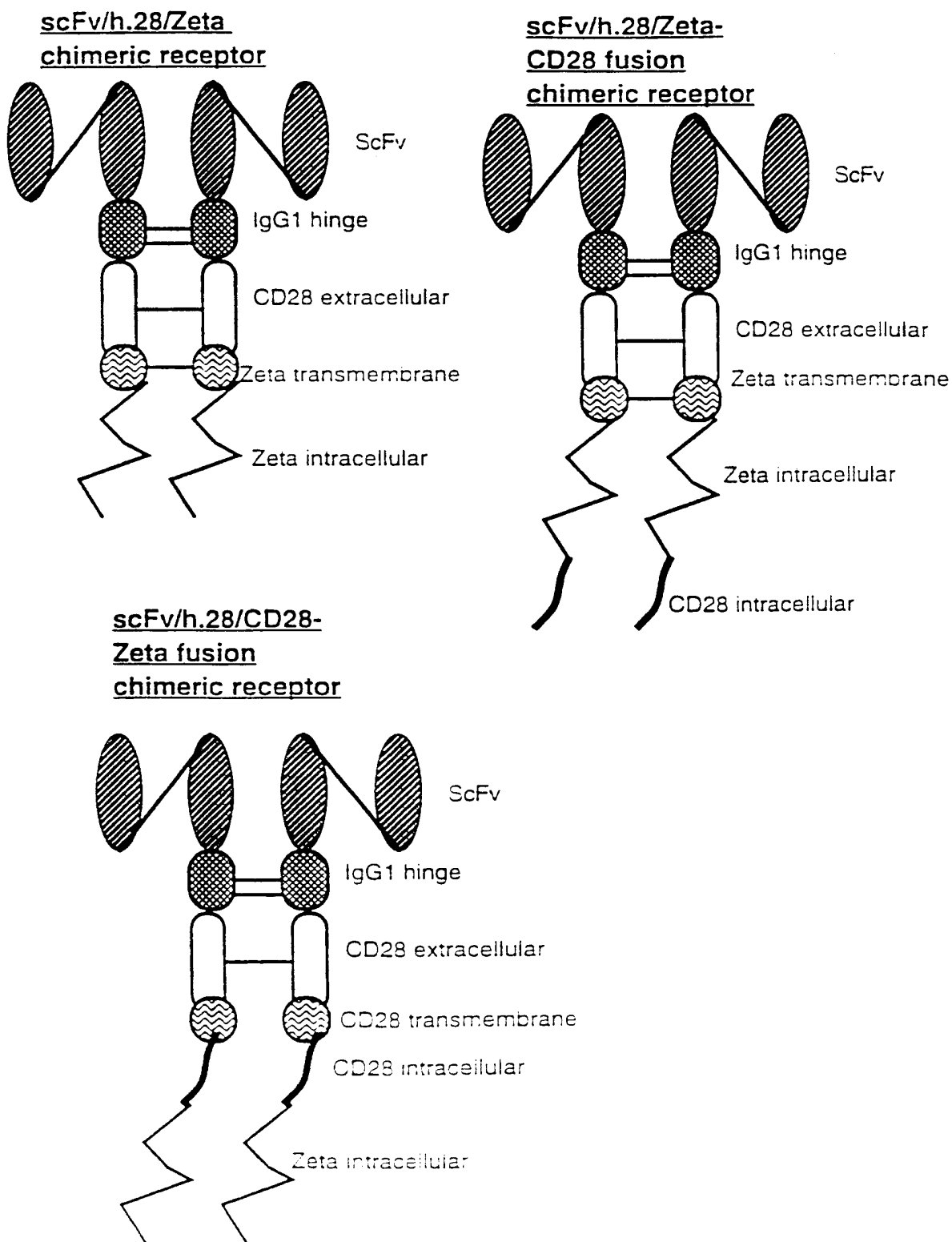
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FIG. 16



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FIG. 17



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FIG. 18  
Surface expression of CD28-chimeras  
in transfected Jurakat cell lines determined  
by FITC-CD33 staining

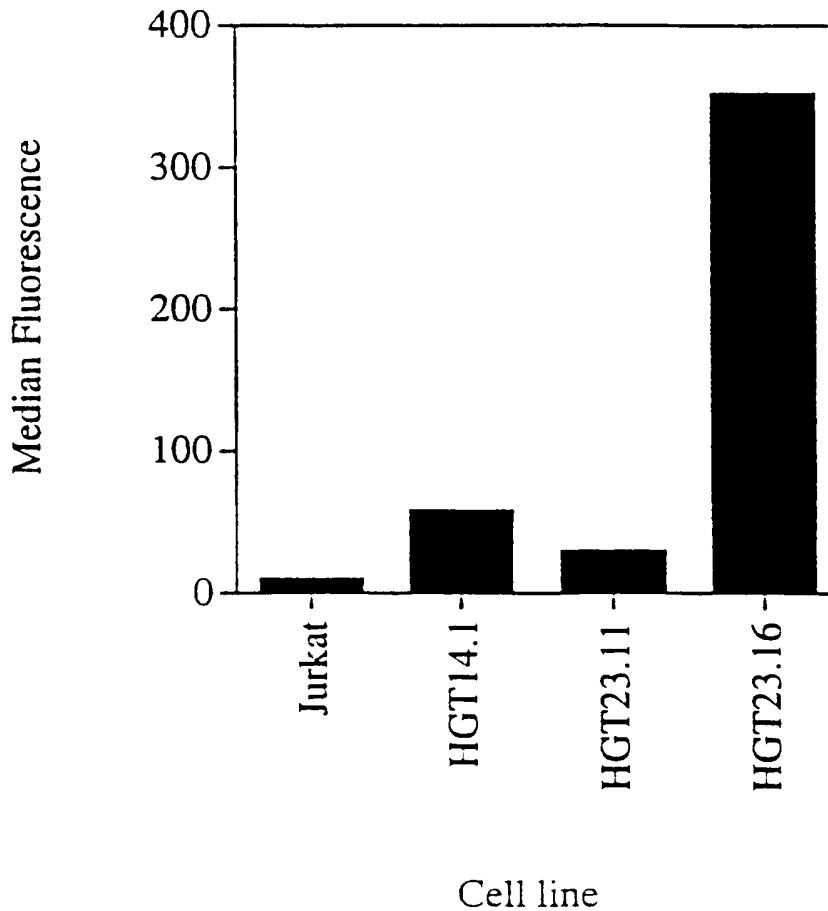
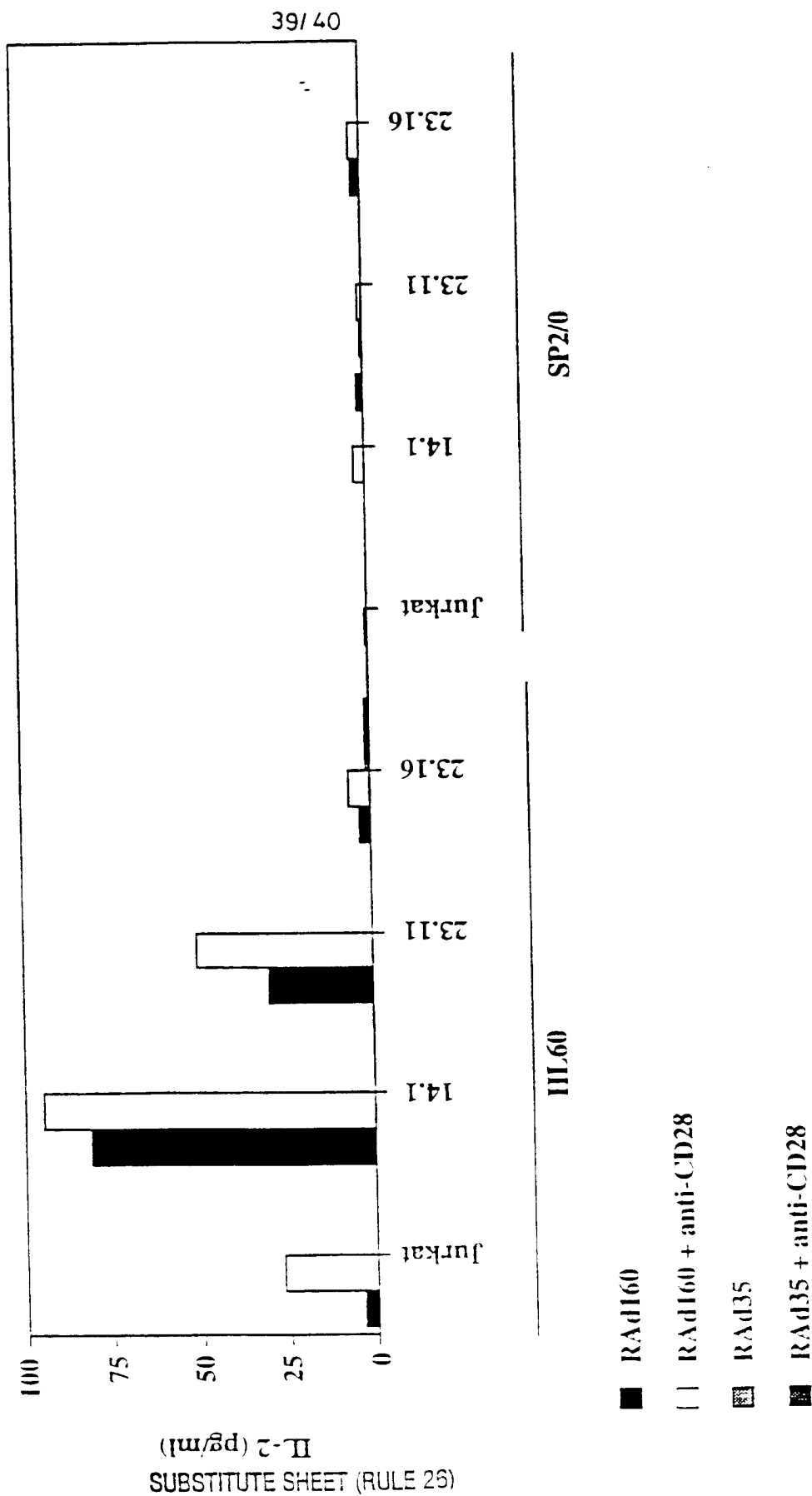


FIG. 19  
IL-2 production by Jurkat cell lines expressing  
p67-CD28 chimeras on infection with RAd160  
stimulated with target cells



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FIG. 20  
**51Cr Release Assay**  
Adenovirus infected CD8+ve peripheral  
blood lymphocytes with HL60 target cells

